

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model

Run on: July 9, 2004, 18:07:37 ; Search time 4046 Seconds  
(without alignments)  
16047.421 Million cell updates/sec

Title: US-09-914-098-55  
Perfect score: 1498  
Sequence: 1 gcacgaggttcggttgctg.....aaaaaaaaaaaaaaaaact 1498

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vi:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rod:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

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3	652.8	43.6	1170	6	BD224663 Novel pla
4	652.8	43.6	1615	8	BNLPAAT
5	651.4	43.5	1480	8	AY084461
6	642.2	42.9	1515	6	A52744 Sequence 3
7	642.2	42.9	1515	6	AR349252
8	640.6	42.8	1486	8	LDAGPATMR
9	548.8	36.6	1514	6	A38840
10	548.8	36.6	1514	6	AR062686
11	548.8	36.6	1514	6	AR135355
12	548.8	36.6	1518	8	ZM1AG3PAT
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23	121.8	8.1	1577	9	BC011971
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33	120.2	8.0	2377	9	BC063552
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41	113.8	7.6	1868	10	AB067572
42	112.8	7.5	3378	10	BC058519
43	112.8	7.5	3379	10	BC052382
44	110.4	7.4	3955	9	AK125804
45	108.6	7.2	1523	6	BD265489

ALIGNMENTS

RESULT 1  
AF213937  
LOCUS  
DEFINITION  
Prunus dulcis 1-acyl-sn-glycerol-3-phosphate acyltransferase mRNA,  
complete cds.  
ACCESSION  
AF213937  
VERSION  
AF213937.1  
KEYWORDS  
Prunus dulcis (almond)  
Prunus dulcis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
1 (bases 1 to 1396)  
REFERENCE  
AUTHORS  
Campalans,A., Pages,M. and Messeguer,R.



Db	137	GGGTAATCTTTGAAATTTGGTGGAGGCCAATGGGATCCAGCTCGGGCTGTGATTGTACC	196
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Qy	218	TGTCGTCGTAAGCCGGTGTGCAAAAGTTTGTACAGAAAGGATCAACCCGGGTAGTAGCAGA	277
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Qy	398	TCACAGAGTGATATTGATTTGGCTTGGTGGATGGGTTTCAGCTCAGCGTTTCAGGTTGTCT	457
Db	437	CCACAGAGTGATATTGATTTGGCTTGGTGGATGGGTTTGGCCAGAGATCAGGCTGCCT	496
Qy	458	TGGCAGCACTCTAGCTGTGATGAAGAAATCTTCAAAAGTTTCTGCCGGTCATTGGCTGGTC	517
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Qy	638	AGAAGGAACGCGTTTACACAGGCCAAACTATTAGCTGCTCAGGAATATGCCACTTCCAC	697
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Qy	698	TGGATTGCTGTTTCTAGAAATGTTTGTGATTTCCAGAACTAAGGGTTTGTCTTCTGCAGT	757
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Qy	758	AAGTCATATGGGCTCATTTGTTCTCTGCCATTTATGATGTAACAGTAGCCATCCCTTAAGAG	817
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Qy	818	TTCCCTGCTCTACAAATGCTAAGACTCTTCAAGGGACAACTTCAGTGGTGCATGTTCA	877
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Qy	878	TATCAAGAGGCAATTTGATGAAGGAACCTGCCAGATACAGATGAGGCTGTTGCTCAATGGTG	937
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BD224663			
LOCUS	BD224663	Novel plant acyltransferases.	
DEFINITION	BD224663		
ACCESSION	BD224663.1	GI:33034433	
VERSION	JP 2002525105-A/12.		
KEYWORDS	Arabidopsis sp.		
SOURCE	Arabidopsis sp.		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi		
REFERENCE	1 (bases 1 to 1170)		
AUTHORS	Lassner,M.W., Emig,R.A., Ruezinsky,D.M. and Eenennaam,A.V.		
TITLE	Novel plant acyltransferases		
JOURNAL	Patent: JP 2002525105-A 12 13-AUG-2002;		
COMMENT	CALGENE LLC		
	OS Arabidopsis sp.		
	PN JP 2002525105-A/12		
	PD 13-AUG-2002		
	PF 24-SEP-1999 JP 2000572337		
	PR 25-SEP-1998 US 60/101939		
	PI MICHAEL W LASSNER,ROBIN A EMIG,DIANE M RUEZINSKY,ALISON VAN		
	PI EENENNAAM		
	PC C12N15/09,A01H5/00,C12N5/10//C12N9/10,C12N15/00,C12N5/00 CC		
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FH Key	Location/Qualifiers		
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FT	/organism='Arabidopsis sp.'		
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Matches 825;	Conservative	0;	Mismatches 287;	Indels 0;
				Gaps 0

QY	138	GCAGCGCCGTTGGTACCAATTTGGGCCCTGCTCTTCTTCGCCCTCCGGCCCTCTTGTTAAAT	197
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QY	438	GCTCAGCGTTCAGGTTGTCTTGGCAGCACTCTAGCTGTGATGAAGAAATCTTCAAAGTTT	497
Db	310	GCTCAGCGGTCAAGTTTGCTGGGAAGCGCATTAGCTGTAAATGAAGAAAGTCTTCCAAATTC	369
QY	498	CTGCCGGTCATTGGCTGGTCAATGATGGTTTTCTGAGTATCTTTTTCTGGAGAGAAGTTGG	557
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AY084461 1480 bp mRNA linear PLN 27-MAR-2003  
Arabidopsis thaliana clone 108727 mRNA, complete sequence.  
AY084461  
AY084461.1 GI:21403171  
FLI CDNA.  
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Arabidopsis thaliana  
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 1480)  
Haas,B.J., Volfovsky,N., Town,C.D., Troukhan,M., Alexandrov,N.,  
Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.  
Full-length messenger RNA sequences greatly improve genome  
annotation  
Genome Biol. 3 (6), RESEARCH0029 (2002)  
2208475  
12093376  
2 (bases 1 to 1480)  
Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and  
Feldmann,K.  
Full-length cDNA from Arabidopsis thaliana  
Unpublished  
3 (bases 1 to 1480)  
Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and  
Feldmann,K.  
Direct Submission  
Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,  
Malibu, CA 90265, USA  
This clone sequence is one of 5,000 Ceres full-length cDNAs made

available to TIGR and Genbank. The following quality assessment of  
this set was done by comparison with known proteins: two percent of  
the clones are estimated to be 5'-truncated; less than one percent  
are 3'-truncated; approximately two percent represent alternative  
splice variants, including unspliced introns and spliced exons; one  
percent may contain premature stop codons; five percent may have  
frame shifts in a coding region. A sequence is considered to be  
5'-truncated if it lacks the translation initiation start (ATG). A  
sequence is considered to be 3'-truncated if it lacks the  
C-terminal end of the encoded protein. Please note that these cDNA  
sequences are derived from the Ws or Laer ecotypes and therefore  
may contain polymorphisms when compared to sequences from Col-0.  
Genset carried out the library production and sequencing of the  
full-length clones. Ceres, Inc. carried out the clustering of the  
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FEATURES

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CDS

ORIGIN

Query Match 43.5%; Score 651.4; DB 8; Length 1480;  
Best Local Similarity 74.1%; Pred. No. 2e-150;  
Matches 824; Conservative 0; Mismatches 288; Indels 0; Gaps 0;  
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RESULT 6  
A52744  
LOCUS A52744 1515 bp DNA linear PAT 12-DEC-1997  
DEFINITION Sequence 3 from Patent WO9624674.  
ACCESSION A52744  
VERSION A52744.1 GI:2851784  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Slabas,A.R., Brown,A.P., Brough,C., Louise and Kroon,J.T.  
TITLE DNA SEQUENCE ENCODING PLANT 2-ACYLTRANSFERASE  
JOURNAL Patent: WO 9624674-A 3 15-AUG-1996;  
GENE SHEARS PTY LTD (AU)  
COMMENT Other publication AU 4669096 960827.  
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Query Match 42.9%; Score 642.2; DB 6; Length 1515;  
Best Local Similarity 73.4%; Pred. No. 3.9e-148;  
Matches 821; Conservative 0; Mismatches 298; Indels 0; Gaps 0;  
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Db 462 GTGACATTGACTGGCTCATTTGGATGGGTTCTAGCACAGCGATGCGGCTGCTCAGTTCTT 521  
QY 466 CTCTAGCTGTGATGAAGAAATCTTCAAAGTTTCTGCGGTCATTTGGTGGTCAATGTGT 525  
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QY 526 TTTCTGAGTATCTTTTCTGGAGAGAAAGTTGGGCCAAGGATGAAAGCATTAAGTCAG 585  
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QY 586 GCATCCAGCGACTGAGTGAATTTCCCTCTTCCCTTTTGGCTAGCTCTCTTTGTAGAAGAA 645  
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Db 1242 TAGCTTCTTCCAGTCAGAGCAATTAACCCCGCAAGA 1280

RESULT 7

AR349252

LOCUS AR349252 1515 bp mRNA linear PAT 17-AUG-2003

DEFINITION Sequence 3 from patent US 6583340.

ACCESSION AR349252

VERSION AR349252.1 GI:33749968

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1515)

AUTHORS Slabas,A.R., Brown,A.P., Brough,C.L. and Kroon,J.T.M.

TITLE DNA sequence encoding plant 2-acyltransferase

JOURNAL Patent: US 6583340-A 3 24-JUN-2003;

FEATURES

source Location/Qualifiers

1..1515

/organism="unknown"

/mol\_type="mRNA"

ORIGIN

Query Match 42.9%; Score 642.2; DB 6; Length 1515;

Best Local Similarity 73.4%; Pred. No. 3.9e-148;

Matches 821; Conservative 0; Mismatches 298; Indels 0; Gaps 0;

Qy 106 TGGGCTGGCTGGGCTGGGCTATTTGACAGAGCGGCGGTGGTACCATTTGGGCC 165

Db 162 TAGCCGAGCTAAAGCTGCCATGGCGATCCCTGTCAGCTTTTCATCGTACCAATAAGTC 221

Qy 166 TGCTCTCTTTCGCCCTCCGGCTCTCTGTTAACTCATTTCCAGGCAATATGCTATGCTCG 225

Db 222 TTCTCTTTTTCATGTCAGGCCTCGTTGTCAATTTTCATTCAGGCGAGTCTTCTATGTTCT 281

Qy 226 TAAGCCCGGTGTCGAAAAAGTTTGTACAGAGGATCAACCGGTAGTAGCAGAGCTCTTGT 285

Db 282 TTCGGCCTATTTCTAAGGACACATACAGAGGATCAATACGTTGGTGGCAGAAATGTTGT 341

Qy 286 GGCTGGAGCTTGATGGCTTATTGATGGTGGGAGGAGTTAAGGTCCAAATATTCACAG 345

Db 342 GGCTAGAACTTGTATGGGTCAATGATGGTGGGAGGCGTTAAGGTCCAATTATATACTG 401

Qy 346 ATCATGAAACCTTTCGTTTAAATGGGTAAAGAGCATGCACCTTGTGATAAGCAATCACAG 405

Db 402 ATACTGAGTCTTTCGCTCTAATGGGTAAAGAACATGCACCTCTTAATATGCAACCCAG 461

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Db 522 CAATAGCTGTTATGAAGAAGTCATCCAAATTTCTCCGGTAATAGGTTGGTCTATGTGGT 581

Qy 526 TTTCTGAGTATCTTTTCTGGAGAGAGTTGGGCCAAGGATGAAGCACATTAAGTCAG 585

Db 582 TTTCCGAATATCTCTTCTCGAGAGGAACCTGGGCCAAAGATGAACAACATTTAAAGTCAG 641

Qy 586 GCATCCAGCGACTGAGTGATTTCCCTCTTCCCTTTTGGCTAGCTCTCTTTGTAGAAGGAA 645

Db 642 GTCTCCAGCGGCTGAATGACTTCCCTAAGCCTTTTGGTTAGCTCTGTTTGTGAAGGAA 701

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Db 702 CTCGTTTACAGAAAGCAAAACTTCTAGCTGCTCAGGAATATGCAGCCTCTGCAGGATTAC 761

Qy 706 CTGTTCTCTAGAAATGTTTGTATTCCAAAGAACTAAGGGTTTGTGTTCTGCAGTAAGTCATA 765

Db 762 CCGTGGCTCGAAATGTTCTGATTCTCGTACGAAGGGCTTTGTGTCAGCCGTTAGTAACA 821

Qy 766 TGCCTCATTTTGTCTGCCATTATATGATGTAACAGTAGCCATCCCTAAGAGTTCCCTCTG 825

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Qy 1126 AGGTGTTGCAATTTTCAGCTTTTGGTTTGGCAGTTGTTACTGCACTTATGCAAAATCTGA 1185

Db 1182 AGGTATGATGATACGACATTCGTTCTGGGAATCGTGACCGCCTTATGCACATCTGA 1241

Qy 1186 TTCAATTTCTCACAGTCAGAGCGTTCAAACCCGGCCAAGA 1224

Db 1242 TAGCTTCTTCCAGTCAGAGCAATTAACCCCGCAAGA 1280

RESULT 8

LDAGPATMR

LOCUS L.douglasii mRNA for 1-acyl-sn-glycerol-3-phosphate acyltransferase 1486 bp mRNA linear PLN 17-NOV-1995

DEFINITION (putative).

ACCESSION Z48730

VERSION Z48730.1 GI:1067137

KEYWORDS 1-acyl-sn-glycerol-3-phosphate acyltransferase.

SOURCE Limnanthes douglasii (Douglas's meadowfoam)

ORGANISM Limnanthes douglasii

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Limnanthaceae; Limnanthes.

1 (bases 1 to 1486)

Brown,A.P., Brough,C.L., Kroon,J.T. and Slabas,A.R.

Identification of a cDNA that encodes a

1-acyl-sn-glycerol-3-phosphate acyltransferase from Limnanthes douglasii

Plant Mol. Biol. 29 (2), 267-278 (1995)

96046746

7579178

2 (bases 1 to 1486)

Brown,A.P., Brough,C.L., Kroon,J.T. and Slabas,A.R.

Identification of a cDNA that encodes a

1-acyl-sn-glycerol-3-phosphate acyltransferase from Limnanthes douglasii

Unpublished

3 (bases 1 to 1486)

Brough,C.L.

Direct Submission



VAFTAAGMALVTGVMHVFIMFSQAERSSSARAARNRVKKE"									
ORIGIN									
Query Match 36.6%; Score 548.8; DB 6; Length 1514; Best Local Similarity 68.8%; Pred. No. 5.5e-125; Matches 770; Conservative 0; Mismatches 347; Indels 3; Gaps 1;									
QY	104	GCTGGGCTGGGCTGGGCTGGGCATGGCTATTGTCAGAGCGGCCGCTGGTGGTACCATGGG	163						
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QY	164	CCTGCTCTTCTTCGCCCTCCGGCTCTCTTGTAAATCTCAATTCAGGCAATATGCTATGCT	223						
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QY	524	GTTTCTGAGTATCTTTTCTGGAGAGAAAGTTTGTACAGAAAGGATCAACCGGGTAGTAGCAGAGCTCTT	583						
Db	528	GTTTGCAGAGTACCTCTTTTGGAAAGGAGCTGGGCCAAGGATGAAGAAGCACTAAAGTG	587						
QY	584	AGGCATCCAGCGACTGAGTGATTTCCCTCTTCCCTTTTGGCTAGCTCTCTTTGTAGAAGG	643						
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QY	1004	TCAAGAGCTGCAGGATACCTGGTCGACCAATAAAGTCTCTTCTGGTGTATATCTTGGGC	1063						
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DEFINITION Sequence 1 from patent US 5843739.									
ACCESSION AR062686									
VERSION AR062686.1 GI:5990377									
KEYWORDS Unknown.									
SOURCE Unknown.									
ORGANISM Unknown.									
REFERENCE 1 (bases 1 to 1514)									
AUTHORS Slabas,A.Ryszard. and Brown,A.Paul.									
TITLE DNA encoding 2-acyltransferases									
JOURNAL Patent: US 5843739-A 1 01-DEC-1998;									
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ORIGIN									
Query Match 36.6%; Score 548.8; DB 6; Length 1514; Best Local Similarity 68.8%; Pred. No. 5.5e-125; Matches 770; Conservative 0; Mismatches 347; Indels 3; Gaps 1;									
QY	104	GCTGGCTGGGCTGGGCTGGGCATGGCTATTGTCAGAGCGGCCGCTGGTGGTACCATGGG	163						
Db	108	GCGGCGCGCGCGCGCGCGATGGCGATGGCGATCCCGCTCGTCTGCTCGTCCCGCTCGG	167						
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QY	404	AAGTGATATTGATTGGCTTGTGGATGGGTTTCAGCTCAGCGTTTCAGGTTGCTTGGCAG	463						
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QY	464	CACCTAGCTGTGATGAAGAAATCTTCAAAGTTTCTGCCGGTCAATTGGCTGGTCAATGTG	523						
Db	468	TACACTTGTCTGTATGAAGAAGTCAATCCAGTTCTCTCCAGTTATTGGCTGGTCAATGTG	527						
QY	524	GTTTCTGAGTATCTTTTCTGGAGAGAAAGTTTGGGCCAAGGATGAAGAAGCACTAAAGTG	583						
Db	528	GTTTGCAGAGTACCTCTTTTGGAAAGGAGCTGGGCCAAGGATGAAGAAGCACTAAAGTG	587						
QY	584	AGGCATCCAGCGACTGAGTGATTTCCCTCTTCCCTTTTGGCTAGCTCTCTTTGTAGAAGG	643						
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QY	644	AACGCGTTTACACAGGCCAAACTATTAGCTGCTCAGGAATATGCCACTTCCACTGGATT	703						
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QY	884	GAGGCATTTGATGAAGGAACTGCCAGATACAGATCAGGCTGTTGTCTCAATGGTGTGAGA	943						
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QY	944	TATATTGTGGCCCAAGGATGCTTTGTAGACAAACATATGGCTGAGGGTACTTTTAGTGA	1003						
Db	948	CATTTTGTGGCAAGGATGCCCTTACTGGACAAGCATTTGGCAACAGGCACCTT---CGA	1004						
QY	1004	TCAAGAGCTGCAGGATACCTGGTCGACCAATAAAGTCTCTTCTGGTGTATATCTTGGGC	1063						
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Db 648 TACTCGCTTTACTCCAGCAAAAGCTTCTCGAGCTCAGGAATATGCGGCTCCAGGGCTT 707  
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ACCESSION AR135355  
VERSION AR135355.1 GI:14124260  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1514)  
AUTHORS Slabas,A.Ryszard, and Brown,A.Paul.  
TITLE Plant expressing 2-acyltransferase  
JOURNAL Patent: US 6194640-A 1 27-FEB-2001;  
FEATURES  
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ORIGIN  
Query Match 36.6%; Score 548.8; DB 6; Length 1514;  
Best Local Similarity 68.8%; Pred. No. 5.5e-125;  
Matches 770; Conservative 0; Mismatches 347; Indels 3; Gaps 1;  
QY 104 GCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 163  
Db 108 GCGGCG 167  
QY 164 CCTGCTCTTCTTCCGCTCCGCGCTCTGTTAAATCTCATTCAGCAATATGCTATGCTG 223  
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QY 224 CGTAAGCCCGGTGCGAAAGTTTGTACAGAAGGATCAACCGGGTAGTAGCAGAGCTCTT 283

Db 228 GATAAGGCCCTTTTTCGAAGAGCTTCTACCCGTCGGATCAACAGATTCTTTGGCCGAGCTGCT 287  
QY 284 GTGGCTGGAGCTTGTATGGCTTATTTGATTGGTGGGCGAGGATTAAGGTCCAAATATTTCAC 343  
Db 288 GTGGCTTCAGCTTGTCTGGGTGGTGGACTGGTGGGCGAGGTAAAGTAACTGATGCATGC 347  
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QY 764 TATCGCTCATTTGTTCTGCGCATTTATGATGTAACAGTAGCCATCCCTAAGAGTTCCCTC 823  
Db 768 TATCGAGATTTTGTTCAGGCCATTTATGATACAACTGTAATAGTCCCTAAAGATTCCCTC 827  
QY 824 TGCTCCTACAAATGCTAAGACTCTTTCAGGGGCAACCTTCAGTGGTGCATGTTTCAATCAA 883  
Db 828 TCAACCAACAATGCTGCGGATTTTGAAAGGCAATCATCATGATACATGTCGCGATGAA 887  
QY 884 GAGGCATTTGATGAAGAACTGCTGCGCATACAGATGAGGCTGTTGCTCAATGGTGTGAGA 943  
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QY 944 TATATTTGTCGCAAGGATGCTTTTGTAGACAAACATATGCTGAGGGTACTTTTAGTGA 1003  
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QY 1064 GTGCTGCTGTTGTTGGCGGCTCTGTAAGTTCCTGCAATGCTTCTGTTACTCTCTCTCTG 1123  
Db 1065 GTGCTCCTGCTGTTTGGCGCATCGAGTCTTCAAGTGGACACAGCTTCTGTGCGAGCTG 1124  
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Db 1125 GAGGGGTGTCGGCTTCACTGCGCAGGATGCGCTTGTGACGGGTGTCATGCTGCTTCT 1184  
QY 1184 GATTCAATTTCTCACAGTCAGAGCGTTTCAAAACCCGCCAAG 1223  
Db 1185 CATCATGTTCTCCAGGCTGAGCGGTCGAGCTCAGCCAGG 1224

RESULT 12  
ZM1AG3PAT  
LOCUS ZM1AG3PAT 1518 bp mRNA linear PLN 17-NOV-1994  
DEFINITION Z.mays (Black Mexican Sweet) mRNA for 1-acyl-glycerol-3-phosphate  
acyltransferase (putative).  
ACCESSION Z29518

229518.1 GI:575959  
1-acyl-glycerol-3-phosphate acyltransferase.  
Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 1518)  
Brown, A.P., Coleman, J., Tomney, A.M., Watson, M.D. and Slabas, A.R.  
Isolation and characterisation of a maize cDNA that complements a  
1-acyl sn-glycerol-3-phosphate acyltransferase mutant of  
Escherichia coli and encodes a protein which has similarities to  
other acyltransferases  
Plant Mol. Biol. 26 (1), 211-223 (1994)  
95035993  
794871  
2 (bases 1 to 1518)  
Brown, A.P.  
Direct Submission  
Submitted (18-JAN-1994) Adrian P Brown, Biological Sciences,  
University of Durham, South, Road, Durham, County Durham, DH1 3LE,  
U.K  
Location/Qualifiers  
1. 1518  
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INRFLAELLWLQVVDWVAGVKVQLHDEETYSMGKEHALIISNHRSDIDWLIGW  
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VAFTAAGMALVTGVHVFIMFSQAERSSSARAARNVKE"  
ORIGIN  
Query Match 36.6%; Score 548.8; DB 8; Length 1518;  
Best Local Similarity 68.8%; Pred. No. 5.5e-125;  
Matches 770; Conservative 0; Mismatches 347; Indels 3; Gaps 1;  
QY 104 GCTGGCTGGCTGGCTGGCTGGCTGGCTATTGACAGCGCGCGTGGTGATGGG 163  
DB 111 GCGGCGCGCGCGCGCGCGCGCGATGCGATCCGCTCGTCTCGTCTCGCTCGG 170  
QY 164 CCGTCTCTCTCGCTCGCGCGCTCTCTGTTAATCTCATTACGCAATATGCTATGCT 223  
DB 171 CCTGCTCTCTCTCTCGCGCGCTCATGCTCAACGCCATCCAGCGCGTCTATTGTGAC 230  
QY 224 CGTAAGCGCGGTGCGAAAGATTGTTACAGAGGATCAACCGGGTAGTAGCAGAGCTCTT 283  
DB 231 GATAAGCGCGCTTTTCGAAGAGCTTCTACCGTCGGATCAACAGATCTTTGGCCGAGCTGCT 290  
QY 284 GTGGCTGAGCTTGTATGGCTTATGATTGGTGGCAGGAGTTAAGGTCCAATATTAC 343  
DB 291 GTGGCTGAGCTTGTCTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 350  
QY 344 AGATCATGAACCTTTCGTTTAAATGGGTAAGAGCATGCATCTGTGATAAGCAATCACAG 403  
DB 351 AGATGAGGAACTTACAGATCAATGGGTAAGAGCATGCATCATCATATCAATCATCG 410

QY 404 AAGTGATATTGATTGGCTTGGATGGGTTTCAGCTCAGCGTTTCAGGTTGTTCTTGGCAG 463  
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QY 464 CACTCTAGCTGTGATGAAGAAATCTTCAAAGTTTCTGCCGGTTCATTGGCTGGTCAATG 523  
DB 471 TACACTTGTCTGTCATGAAGAGTCAATCCAAAGTTTCTTCCAGTTTATTGGCTGGTCAATG 530  
QY 524 GTTTTCTGAGTATCTTTTCTGGAGAGAGTGGGCCAAGGATGAAGACACATTAAGTC 583  
DB 531 GTTTGACAGTACCTCTTTTGGAAAGGAGTGGGCCAAGGATGAAGACACATTAAGTC 590  
QY 584 AGGCATCCAGGACTGAGTGAATTTCCCTCTTCCCTTTTGGCTAGCTCTCTTTGTAGAAG 643  
DB 591 GGGTCTCCAAAGGTTGAAGACTTCCCTAGACCATTTTGGCTAGCTCTTTTCGTCGAGGG 650  
QY 644 AACGCGTTTACACAGGCGCAAACTATTAGCTGCTCAGGAATATGCCACTTCCACTGGATT 703  
DB 651 TACTCGCTTTACTCCAGCAAAAGCTTCTCGCAGCTCAGGAATATGCCGCTCCAGGGCTT 710  
QY 704 GCCTGTTTCTAGAAATGTTTGAATTTCCAAAGAACTAAGGGTTTGTCTTGCAAGTAA 763  
DB 711 ACCGGCTCTAGAAATGTTTGAATTTCCAAAGAACTAAGGGTTTGTCTTGCAAGTAA 770  
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QY 944 TATATTTGTGGCAAGGATGCTTTGTTAGACCAATAAAGTCTCTTCTGTTAGTTATCTT 1003  
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QY 1004 TCAAGAGCTGCAGGATACCTGTCGACCAATAAAGTCTCTTCTGTTAGTTATCTTGGGC 1063  
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DB 1128 GAGGGTGTGGCGTTTCACTCGCGAGGATGGCGTTGTGACGGGTGTCATGCTATGCTT 1187  
QY 1184 GATTCAATCTCAGCTCAGAGCGTTCAAAACCCGCCCAAG 1223  
DB 1188 CATCATGTTCTCCAGGCTGAGCGGTGAGCTCAGCCAGG 1227  
RESULT 13  
BT009239  
LOCUS  
DEFINITION  
Triticum aestivum clone wlkl.pk0004.e7.fis, full insert mRNA  
sequence.  
ACCESSION  
BT009239  
VERSION  
BT009239.1 GI:32128790  
KEYWORDS  
FLI\_CDNA.  
SOURCE  
Triticum aestivum (bread wheat)  
ORGANISM  
Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooideae; Triticeae; Triticum.  
1 (bases 1 to 1415)  
Tingey, S.V., Wolters, P., Powell, W., Dolan, M., Miao, G.-H.,  
Caraher, N.R., Hanafey, M.K. and Hainey, C.F.



Db 209 TCAGAGGTGAGTTGCTAGGAGCGCATAGTGTGATGAGAAAGTCTTCCAAATTTCT 268  
Qy 500 GCCGTCATTGGCTCAATGTGTTTCTGAGTATCTTTTCTGGAGAAAGTTGGGC 559  
Db 269 CCCAGTCATAGGCTGCTCAATGTGTTTCTCCGAGTATCTGTTCTTGAAGAAATTTGGC 328  
Qy 560 CAAGATGAAAGCACATTAAAGTCAGGCAATCCAGCGCATGAGTGAATTCCTCTTCCCTT 619  
Db 329 AAAGATGAAAGCACTTTAAAGTCAGGCTCTTCAAGCGTTGAACGACTTCCACGGCTTT 388  
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Qy 680 GGAATATGCCACTTCCACTGGATTGCTGCTTCTCTAGAAATGTTTGTATCCAAAGAACATA 739  
Db 449 AGAGTACGACGCTCTCTGAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 508  
Qy 740 GGGTTTGTGTTCTGAGTAAGTCATATGCGCTCATTTGTTCTGCTGCTGCTGCTGCTGCTGCT 799  
Db 509 AGGATTTGTGTCAGCTGTTAGTAACATGCGTTCTTATTTGTCAGGCCATATATGATATGAC 568  
Qy 800 AGTAGCATCCCTAAGAGTTCCCTGCTCTCTAAGTCTAAGACTCTTCAAGGGGACAAAC 859  
Db 569 CGTGGCTATTCAAAAAATCTTCCACCCCAAGCATGCTAAGACTATTCAAGGACAAAC 628  
Qy 860 TTCAGTGGTGCATGTTTCAATCAAGAGGCAATTTGATGAAGGAAGTCCAGATACAGATGA 919  
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Qy 980 TATGCTGAGGTTACTTTTATGATCAAGAGCTGTCAGGATGCTGTCGACCAATAAAGTC 1039  
Db 749 CATAGTGCAGACACTTTTCCGCGTCAAGAAAGCAAGCAATGCGCGTCCCATAAAGTC 808  
Qy 1040 TCTTCTGGTAGTTATATCTTGGCGGTGCTGCTGTTGTTGGGGTCTGTAAAGTTCTCTGCA 1099  
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Qy 1100 ATGGTCTTCTGTTACTCTCTTCTGGAAGGTTGTCATTTTTCAGCTTTTGGTGGCAGT 1159  
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Qy 1160 TGTACTGCACTTATGCAAAATCTGATTCATTTCTCAGTCAGAGCGTTTCAAAACCGGC 1219  
Db 929 CATCACTCTCTGATGAGATCTTGTATCCGCTCTCTCAGTCGGAGCGTTCAACACCTGC 988  
Qy 1220 CAAGATCGTGCCTGCAAAAGTCAAAAAACAA 1249  
Db 989 CAAAGTCGCTCCAGCAAGCCAAAGGACAA 1018

RESULT 15  
AF479037  
LOCUS AF479037 714 bp mRNA linear PLN 02-JUL-2003  
DEFINITION Triticum aestivum 1-acyl-glycerol-3-phosphate acyltransferase mRNA, partial cds.  
ACCESSION AF479037  
VERSION AF479037.1 GI:32400848  
KEYWORDS Triticum aestivum (bread wheat)  
SOURCE Triticum aestivum  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.  
REFERENCE 1 (bases 1 to 714)  
AUTHORS Li, J. R., Wang, F., Li, Q. Z. and Zhang, X. S.  
TITLE Gene isolation and expression of 1-acyl-glycerol-3-phosphate acyltransferase  
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 714)  
AUTHORS Li, J. R., Wang, F., Li, Q. Z. and Zhang, X. S.  
TITLE Direct Submission  
JOURNAL Submitted (29-JAN-2002) College of Life Science, Shandong Agricultural University, Dai Zong Street 61, Taian, Shandong 271018, P.R. China  
FEATURES  
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ORIGIN

Query Match 22.1%; Score 331; DB 8; Length 714;  
Best local Similarity 71.6%; Pred. No. 5e-71;  
Matches 447; Conservative 0; Mismatches 176; Indels 1; Gaps 1;  
Qy 377 GCATGCACCTTGTGATAAGCAATCACAGAGTGTATGATTTGGCTTGGATGGGTTTC 436  
Db 3 GGACGCCCTTCTAATATCCAAATCATCGAAGTGACATTGGCTGGTGGATGATTTT 62  
Qy 437 AGCTCAGCGTTTCAGGTTGTCTTGGCAGCACTCTAGCTGTGATGAAGAAATCTTCAAAGTT 496  
Db 63 AGCAGCGTTTCAGGATGCTTGAAGCGCAATAGCTATATGAAGAAATCTTCAAAGTT 122  
Qy 497 TCTGCCGCTCATTTGGTGTCAATGTGTTTCTGAGTATCTTTTCTGGAGAGAGTTG 556  
Db 123 CCTCCAGTTATTTGGTCTCATGTTGTTGAGAAATACCTCTTTTGGAGAGAGCTG 182  
Qy 557 GGCRAAGGATGAAAGCACATTAAGTCAAGGCATCCAGGCATGAGTATTTCCCTCTTC 616  
Db 183 GGCRAAGGATGAAAGAACACTCAATCGGCTCTTCAAAGGTTGAAGACTTCCCGATC 242  
Qy 617 CTTTGGCTAGCTCTCTTTGTAGAGGAGCGGTTTACACAGGCCAACTATTAGCTGC 676  
Db 243 ATTTTGGCTTGGCTTTTGTGAGGGTACAAGATTACTCCAGCAAAACTTTTAGCAGC 302  
Qy 677 TCAGGAATATGCCACTTCCACTGGATTGCTGCTCTCTAGAAATGTTTGTATCCAGAAC 736  
Db 303 TCAAGATATGCAATCTCACAGGGTTTGACAGCGCTTAGGAATGTGCTGATTCACGGAAC 362  
Qy 737 TAAGGGTTTTTCTGCAAGTCAATATGCGCTCATTTGTTCTGCTCCATTTATGATGT 796  
Db 363 AAAGGGATTGTATCAGCTGTAGTATTATGCTGACTTTGTCCCAGCTATCTATGATAC 422  
Qy 797 AACAGTAGCCATCCCTAAGAGTTCCCTGCTCTCTACATGCTAAGACTTCTCAAGGACA 856  
Db 423 AACAGTGATTATCCAGAGATTTCGCTTAAACCAACCAATGCTGCTGATTTCTCAGGGACA 482  
Qy 857 ACCTTCAGTGTGCTATGTTTCATATCAAGAGGCTTTTGTATGAAGGAAGTCCAGATACAGA 916  
Db 483 ATCATCAGTTGTATGTCGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 542  
Qy 917 TGAGGCTGTTGCTCAATGTTGTCGAGATATATTTTGTGGCCAAAGGATGCTTTGTT-AGACA 975  
Db 543 TGAGGATGTTTCAAAATGTTGCAAGACATATTTTGTAGCAAAANGACGCTTATTGGGACA 602  
Qy 976 AACATATGCTGAGGGTACTTTTA 999

Mon Jul 12 10:08:44 2004

us-09-914-098-55.rge

Page 14

Db 603 AACATATAGCAACTGGTCTTTTGA 626

Search completed: July 9, 2004, 21:00:24  
Job time : 4051 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 9, 2004, 18:01:02 ; Search time 467 Seconds  
(without alignments)  
13626.982 Million cell updates/sec

Title: US-09-914-098-55  
Perfect score: 1498  
Sequence: 1 gcaagaggttcggttgctg.....aaaaaaaaaaaaaaaaaact 1498

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002s:\*  
7: Geneseqn2003as:\*  
8: Geneseqn2003bs:\*  
9: Geneseqn2003cs:\*  
10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	672.8	44.9	1702	3	AAA37472 DNA encod
3	652.8	43.6	1170	3	AAA37342 cDNA enco
4	652.8	43.6	1170	3	AAC50510 Arabidops
5	651.4	43.5	1480	3	AAC36124 Arabidops
6	637.4	42.6	1515	2	AAT35205 Limnanthe
7	550.4	36.7	1514	2	AAQ68267 Maize 2-a
8	549.2	36.7	1632	3	AAA64199 Nucleotid
9	525	35.0	1415	3	AAA64201 Nucleotid
10	520.6	34.8	1391	3	AAC50517 Arabidops
11	511.8	34.2	584	3	AAA64183 Nucleotid
12	491	32.8	1131	3	AAC43080 Arabidops
13	448	29.9	1510	3	AAC43788 Zea mays
14	228	15.2	570	3	AAA64184 Nucleotid
15	210.8	14.1	485	3	AAC38209 Zea mays
16	193.2	12.9	784	3	AAA64182 Nucleotid
17	190.6	12.7	312	3	AAA37432 Maize acy
18	150	10.0	279	3	AAA37433 Maize acy
19	150	10.0	279	6	ABL73513 Corn tass
20	145	9.7	304	3	AAA37434 Maize acy
21	132	8.8	259	3	AAA37435 Maize acy
22	129.4	8.6	235	3	AAA37436 Maize acy
23	121.8	8.1	1660	3	AAA51068 Human LPA

24	121.8	8.1	1660	6	AA224423	Aad24423 Human LPA
25	121.8	8.1	1660	8	ABX16124	Abx16124 Human CDN
26	120.2	8.0	1333	3	AAA71493	Aaa71493 Human lys
27	120.2	8.0	1612	4	AAI60735	Aai60735 Human pol
28	120.2	8.0	1769	4	AAI58949	Aai58949 Human pol
29	120.2	8.0	1769	8	ADB48931	Adb48931 Novel hum
30	120.2	8.0	1832	5	AAH75152	Aah75152 Nucleotid
31	120.2	8.0	1960	6	AA224014	Aad24014 Human dru
32	120.2	8.0	3059	4	AA546093	Aas46093 Human DNA
33	120.2	8.0	3060	3	AAA37104	Aaa37104 Human PRO
34	120.2	8.0	3060	4	AAF54413	Aaf54413 Primer #8
35	120.2	8.0	3060	7	ABX78696	Abx78696 Human PRO
36	120.2	8.0	3060	7	ACA75668	Aca75668 Novel hum
37	120.2	8.0	3060	7	ACA71148	Aca71148 Human sec
38	120.2	8.0	3060	7	ACC87676	Acc87676 Human sec
39	120.2	8.0	3060	7	ACC87062	Acc87062 Human sec
40	120.2	8.0	3060	7	ACD04235	AcD04235 Human sec
41	120.2	8.0	3060	7	ACA69566	Aca69566 cDNA enco
42	120.2	8.0	3060	7	ACA90411	Aca90411 Novel hum
43	120.2	8.0	3060	7	ACC89518	Acc89518 Human sec
44	120.2	8.0	3060	7	ACA98309	Aca98309 Novel hum
45	120.2	8.0	3060	7	ACA93951	Aca93951 Human sec

ALIGNMENTS

RESULT 1  
AAA64200  
ID AAA64200 standard; DNA; 1498 BP.  
XX  
AC AAA64200;  
XX  
DT 20-DEC-2000 (first entry)  
XX  
DE Nucleotide sequence of a lysophosphatidic acid acetyltransferase.  
XX  
KW Lysophosphatidic acid acetyltransferase; LPAAT; transgenic plant;  
KW triacylglycerol; oil content; ss.  
XX  
OS Glycine max.  
XX  
FH Key Location/Qualifiers  
FT CDS 126..1259  
FT /\*tag= a  
FT /product= "lysophosphatidic acid acetyltransferase  
FT (LPAAT) isoenzyme"  
XX  
PN WO200049156-A2.  
XX  
XX 24-AUG-2000.  
XX  
PF 22-FEB-2000; 2000WO-US004526.  
XX  
PR 22-FEB-1999; 99US-0121119P.  
XX  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX  
PI Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ, Ripp KG;  
XX WPI; 2000-558300/51.  
DR P-PSDB; AAB08478.  
XX  
PT New nucleic acid fragment encoding a lysophosphatidic acid  
PT acetyltransferase (LPAAT) isozyme, useful for creating transgenic plants  
PT which encode LPAAT at higher or lower levels than normal.  
XX  
PS Claim 39; Page 99; 102pp; English.  
XX  
CC The present sequence encodes a lysophosphatidic acid acetyltransferase  
CC (LPAAT) isoenzyme. The nucleic acid may be used to create transgenic  
CC plants which encode LPAAT at higher or lower levels than normal or in  
CC cell types or developmental stages in which they are not normally found.



(CALJ ) CALGENE LLC.

Lassner MW, Emig RA, Ruezinsky DM, Van Benennaam A;  
WPI; 2000-303447/26.  
P-PSDB; AAY99482.

Novel acyltransferase related proteins useful for altering membrane fluidity in plant cells e.g. to induce chill tolerance.

Example 5; Page 98; 126pp; English.

The invention relates to nucleic acids encoding novel plant acyltransferase-like proteins (AAA37343-A37445) which comprise one of 8 conserved acyltransferase motifs (AAY99474-Y99481). Acyltransferases catalyse the transfer of acyl groups from a donor to a variety of substrates such as glycerides, sterols, stanols and phosphatides. Such enzymes play a key role in lipid synthesis, and thereby affect the characteristics of the plant. For example, cold-hardened plants have different lipid concentrations in the cell membrane compared to non-hardened plants, which makes the membrane more fluid and the plant more tolerant of low temperatures. The nucleic acid sequences of the invention can be used as probes or for expressing acyltransferase-like proteins in host cells e.g., for recombinant protein production. They may be expressed in plant cells to alter the lipid composition of the plant e.g., for the production of chill-resistant plants, or for altering the composition of plant oils. The present sequence represents DNA encoding jojoba lysophosphatidic acid acyltransferase (LPAAT)

Sequence 1702 BP; 435 A; 368 C; 383 G; 514 T; 0 U; 2 Other;

Query Match 44.9%; Score 672.8; DB 3; Length 1702;  
Best Local Similarity 73.7%; Pred. No. 1.9e-165;  
Matches 854; Conservative 0; Mismatches 304; Indels 0; Gaps 0;

QY 98 GGCTGGGCTGGGCTGGGCTGGGCTGGGCTATTCAGCAGCGGCGGTGGTACC 157  
Db 137 GGGTAATCTGAATTTGTTGGTGAGGCCATGGGGATCCAGTCGGCTGATGTACC 196

QY 158 ATTGGGCTGCTCTTCTTCGCTCCGGCTCCTTGTTAATCTCATTGAGGCAATGCTA 217  
Db 197 GCTTGGCTTGCTCTTCTTCTTCTGCTGCTCTTCATCAACTTCATTGAGGCAATTGTTT 256

QY 218 TGTCTGCTGAAGCCGGTGTGCAAAAAGTTTGTACAGAAGGATCAACCGGTAGTAGCAGA 277  
Db 257 TGTCTGCTGTCGGCCACTGTCAAAGNNTACATACAGAAGGATTAACAGGGTGCTGGTGA 316

QY 278 GCTCTTGGCTGGAGCTTGATGGCTTATTAATTTGGTGGGAGGAGTTAAGTCCAAAT 337  
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QY 338 ATTCACAGATCATGAACCTTTCGTTTAAATGGGTAAGAGCATGCACCTTGTGATAAGCAA 397  
Db 377 GTTCACAGATCCTGATACCTTTCGGCTAATGGGTAAGAGCATGCACCTTGTGATATCAA 436

QY 398 TCACAGAAAGTGATATTGATTGGCTTGTGGATGGGTTTCAGCTCAGCGTTTCAGTTGTCT 457  
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QY 458 TGGCAGCACTCTAGCTGTGATGAAGAAATCTTCAAAGTTTCTGCGGCTCATTGGCTGGTC 517  
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QY 518 AATGTGGTTTTCTGAGTATCTTTTTTCTGGAGAGAAGTTGGGCCAAGGATGAAGCACATT 577  
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QY 578 AAGTCAGGCATCCAGCGACTGAGTGATTTCCTCTTCCTTTTGGCTAGCTCTCTTTGT 637  
Db 617 GAAGTTAGGTCTTCAACGCCTCAAGGACTACCCCTCTGCCTTCTTGGTTGGCTCTTTTGT 676

QY 638 AGAAGGAACGGTTTTTACACAGGCCAAACTATTAGCTGCTCAGGAATATGCCACTTCCAC 697

PA (CALJ ) CALGENE LLC.  
XX Lassner MW, Emig RA, Ruezinsky DM, Van Eenennaam A;  
PI WPI; 2000-303447/26.  
XX P-PSDB; AAY99473.  
DR  
XX  
PT Novel acyltransferase related proteins useful for altering membrane  
PT fluidity in plant cells e.g. to induce chill tolerance.  
XX  
XX  
PS Example 5; Page 74-75; 126pp; English.  
XX  
CC The invention relates to nucleic acids encoding novel plant  
CC acyltransferase-like proteins (AAA37343-A37445) which comprise one of 8  
CC conserved acyltransferase motifs (AAY99474-Y99481). Acyltransferases  
CC catalyze the transfer of acyl groups from a donor to a variety of  
CC substrates such as glycerides, sterols, stanols and phosphatides. Such  
CC enzymes play a key role in lipid synthesis, and thereby affect the  
CC characteristics of the plant. For example, cold-hardened plants have  
CC different lipid concentrations in the cell membrane compared to non-  
CC hardened plants, which makes the membrane more fluid and the plant more  
CC tolerant of low temperatures. The nucleic acid sequences of the invention  
CC can be used as probes or for expressing acyltransferase-like proteins in  
CC host cells e.g., for recombinant protein production. They may be  
CC expressed in plant cells to alter the lipid composition of the plant  
CC e.g., for the production of chill-resistant plants, or for altering the  
CC composition of plant oils. Sequences AAA37331-A37342 represent cDNAs  
CC encoding Arabidopsis thaliana acyltransferases ATAT1-ATAT11 and  
CC lysophosphatidic acid acyltransferase ATLPAAT1, respectively  
XX  
SQ Sequence 1170 BP; 306 A; 277 C; 268 G; 319 T; 0 U; 0 Other;  
Query Match 43.6%; Score 652.8; DB 3; Length 1170;  
Best Local Similarity 74.2%; Pred. No. 2.8e-160;  
Matches 825; Conservative 0; Mismatches 287; Indels 0; Gaps 0;  
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Db 10 GCTGCAGCTGTCAATCGTGGCTTTGGGCTTCTCTTCATATCTGGTCTCGTGTCAAT 69  
QY 198 CTCATTACGGCAATATGCTATGTCGTCTAAGCGCGGTGTCGAAAGTTTGTACAGAAG 257  
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QY 258 ATCAACCGGGTAGTAGCAGAGCTCTTGTGGCTGGAGTTGTATGGCTTATTGATGGTGG 317  
Db 130 ATTAACCGGGTGGTTCAGAAACCTTGTGGTGGAGTTGTATGGATGATGTTGCTGGTGG 189  
QY 318 GCAGGAGTTAAGGTCCTAATATTCACAGATCATGAACCTTTTCGTTAATGGGTAAAGAG 377  
Db 190 GCTGGAGTTAAGATCCAAAGTGTGTGTGATAATGAGACCTTCAATCGAATGGGCAAGAA 249  
QY 378 CATGCACCTGTGATAAGCAATCACAGAAGTGATATTGATTTGGCTTGTGGATGGTTTCA 437  
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QY 438 GCTCAGCTTTCAGGTTGCTTGTGGCAGCACTCTAGCTGTGATGAAGAAATCTTCAAAGTTT 497  
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QY 498 CTGCGGCTCATTTGGCTGCTCAATGTGGTTTCTGAGTATCTTTTCTGGAGAGAGTTGG 557  
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Db 430 GCCAAGGATGAAAGCACTCTAAAGTCAGGCTTTAGCGCTTTCAGCGACTTCCCTCGACCT 489  
QY 618 TTTTGGCTAGCTCTCTTTGTAGAAAGAACCGCTTTTACACAGGCAAACTATTAGCTGCT 677  
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QY 918 GAGGCTGTTGCTCAATGGTGTGAGATATATTGTTGGCAAGGATGCTTTGTTAGACAAA 977  
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RESULT 4

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AC AAC50510;  
XX  
DT 18-OCT-2000 (first entry)  
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DE Arabidopsis thaliana DNA fragment SEQ ID NO: 65109.  
XX  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway; metabolic pathway;  
KW promoter; termination sequence; ss.  
OS Arabidopsis thaliana.  
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PN EP1033405-A2.  
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PD 06-SEP-2000.  
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PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.





Db 108 GCGGCGCGGCGCGCGCGCGGCGATGGCGATCCCGCTCGTGTCTGTCGTCTCCGCTCGG 167

QY 164 CCGTCTCTTCTTCGCGCTCCGCGCTCCTTGTAAATCTCATTCAGGCAATATGCTATGTCGT 223

Db 168 CCGTCTCTTCTTCGCGCTCCGCGCTCATCGTCAACGCCATCCAGGCCGCTCTATTGTGAC 227

QY 224 CGTAAGGCGCGGTGTCGAAAGTTGTACAGAAGGATCAACCGGTTAGTACAGAGCTCTT 283

Db 228 GATAAGGCCCTTTTCGAAGAGCTTCTACCGTCGGATCAACAGATTCTTGGCCGAGCTGT 287

QY 284 GTGGCTGAGCTGTATGGCTTATTTGATTTGGTGGCAGGATTAAGTCCAAATATTAC 343

Db 288 GTGGCTTGGCTGTCTGGTGGTGGACTGGTGGCAGGTTTAAAGTACAAGTGCATGC 347

QY 344 AGATCATGAACCTTTTCGTTTAATGGTTAAAGAGCATGCACTTGTGATAAGCAATCACAG 403

Db 348 AGATGAGAAACTTACAGATCAATGGTTAAAGAGCATGCACTCATATCAATCATCG 407

QY 404 AAGTGATATTGATGGCTTGTGGATGGTTTCAGCTCAGCGTTTCAGGTTGTCTTGGCAG 463

Db 408 GAGTGATATTGATGGCTCACTGATGGATTTGGCCAGCGTTTCAGGTTGCCTTGGAG 467

QY 464 CACTCTAGCTGTGATGAAGAAATCTTCAAGTTTCTGCGGTCATTTGGTGGTCAATGTG 523

Db 468 TACACTTGTGTCTCATGAAGAGTCAATCCAGTTCTTCCAGTTATTGGTGGTCAATGTG 527

QY 524 GTTTTCTGATATCTTTTCTGGAGAGAGTTGGCCAGGATGAAGCAATTAAGTC 583

Db 528 GTTTCAGAGTACCTCTTTTGGAAAGAGCTGGCCAGGATGAAGACACATAAGTG 587

QY 584 AGGCATCCAGCGACTGATGATTTCCCTCTTCCCTTTGGCTAGCTCTCTTTGTAGAAG 643

Db 588 GGGTCTCCAAAGGTTGAAGACTTCCCTAGACCAATTTTGGCTAGCTCTTTTCGTCGAGG 647

QY 644 AACGCGTTTACACAGGCCAAACTATTAGCTGTCTCAGGAATATGCCACTTCCACTGGATT 703

Db 648 TACTCGCTTACTCCAGCAAGCTTCTCGAGCTCAGGAATATCGGCGCTCCAGGCTT 707

QY 704 GCCTGTTCTAGAAATGTTTGTATTCGAAGAACTAAGGTTTTTGTTCAGTAACTCA 763

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QY 764 TATGCGCTCATTTGTTCTCGCCATTTATGATGTAAAGTAGCCATCCCTAAGATTCCCC 823

Db 768 TATGCGAGATTTGTTCCAGCCATTTATGATACAACTGTAATAGTCCCTAAGATTCCCC 827

QY 824 TGCTCCTACAATGCTAAGACTCTTCAAGGCAACCTTCAGTGGTGCATGTTTCATATCAA 883

Db 828 TCAACCAACAATGCTCGGATTTTGAAGGGCAATCATCAGTGATACATGTCCGGATGAA 887

QY 884 GAGGCATTTGATGAAGGAAGTCTCCAGATACAGATGAGGCTGTTGCTCAATGGTTCGAGA 943

Db 888 ACGTCATGCAATGATGAGATGCCAAATCAGATGAGGATGTTTCAAAATGGTGTAAAGA 947

QY 944 TATATTGCGCCCAAGGATGCTTTGTTAGACAAACATATGGCTGAGGTTACTTTTAGTGA 1003

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QY 1004 TCAAGAGTGCAGGATACCTGGTCGACCAATAAGTCTCTTCTGGTAGTTATATCTTGGC 1063

Db 1005 TGAGGAGATTAGACCTATTGGCCGCTCCAGTGAATCATTTGCTGGTGACCTGTTCTGTC 1064

QY 1064 GTGTCTGTTGTTGGGGTCTGTAAAGTTCTGTGAATGTTCTGTTACTCTCTTCTCTG 1123

Db 1065 GTGCTCTGCTGTTTGGCGCCATCGAGTTCTTCAAGTGGACACAGCTTCTGTGACGCTG 1124

QY 1124 GAAGGGTGTGCAATTTTCAGCTTTTGGTTGGCAGTTGTTTACTGCACTTATGCAATTTCT 1183

Db 1125 GAGGGTGTGGCGTTTCACTGCGCAGGATGGCGTTGTGACGGGTGTCATGATGCTT 1184

QY 1184 GATTCAATTTCTACAGTCAGAGCGTTTCAACCCCGGCAAG 1223

Db 1185 CATCATGTTTCTCCAGGCTGAGCGGTGAGCTCAGCCAGG 1224

RESULT 8  
AAA64199  
ID AAA64199 standard; DNA; 1632 BP.  
XX  
AC AAA64199;  
XX  
DT 20-DEC-2000 (first entry)  
XX  
DE Nucleotide sequence of a lysophosphatidic acid acetyltransferase.  
XX  
KW Lysophosphatidic acid acetyltransferase; LPAAT; transgenic plant;  
KW triacylglycerol; oil content; ss.  
XX  
OS Oryza sativa.  
XX  
FH Key Location/Qualifiers  
FT CDS 173..1297  
FT /\*tag= a  
FT /product= "lysophosphatidic acid acetyltransferase  
FT (LPAAT) isoenzyme"  
XX  
PN WO200049156-A2.  
XX  
PD 24-AUG-2000.  
XX  
PF 22-FEB-2000; 2000WO-US004526.  
XX  
PR 22-FEB-1999; 99US-0121119P.  
XX  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX  
PI Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ, Ripp KG;  
XX  
DR WPI; 2000-558300/51.  
DR P-PSDB; AAB08477.  
XX  
PT New nucleic acid fragment encoding a lysophosphatidic acid  
PT acetyltransferase (LPAAT) isozyme, useful for creating transgenic plants  
PT which encode LPAAT at higher or lower levels than normal.  
XX  
PS Claim 39; Page 97; 102pp; English.  
XX  
CC The present sequence encodes a lysophosphatidic acid acetyltransferase  
CC (LPAAT) isoenzyme. The nucleic acid may be used to create transgenic  
CC plants which encode LPAAT at higher or lower levels than normal or in  
CC cell types or developmental stages in which they are not normally found.  
CC This would have the effect of altering the level of specific  
CC triacylglycerols in those cells, for e.g. overexpression of an LPAAT  
CC similar to the maize LPAAT will result in higher oil content in the seed,  
CC stem and leaf. LPAAT chimeric genes may be used for co-suppression of  
CC genes encoding LPAAT. The polynucleotides may also be used as probes for  
CC genetically and physically mapping the genes that are a part of, and as  
CC markers for traits linked to those genes  
XX  
SQ Sequence 1632 BP; 407 A; 361 C; 426 G; 438 T; 0 U; 0 Other;

Query Match 36.7%; Score 549.2; DB 3; Length 1632;  
Best Local Similarity 68.7%; Pred. No. 4.2e-133;  
Matches 771; Conservative 0; Mismatches 348; Indels 3; Gaps 1;  
QY 102 GGGCTGGCTGGGCTGGGCTGGGCTGGGCTATTGTCAGCAGCGCGCGTGGTGGTACCATTG 161  
Db 149 GGGCAGGCGAGGCGGCGAGGCGCGGCGGCTCCACTCGTGTCTGTCGTCTCCGCTC 208  
QY 162 GGCCTGCTCTTCTTCGCTCCGCGCTCCTTGTGTTAATCTCATTCAGGCAATATGCTATGTC 221  
Db 209 GGCCTCTCTTCTCTCTCTCCGCGCTCATCATCAACGCCATCCAGCGCGTCTCTGTTCTC 268  
QY 222 GTCGTAAGCGCGGTGTCGAAAGTTGTACAGAAGCATCAACCGGTTAGTAGCAGAGCTC 281  
Db 269 TCGATAAGCGCGGTTCTCGAAGAGCTTGTTACCGCGGATCAACAGGTTCTTTGGCCGAGCTG 328



XX Nucleotide sequence of a lysophosphatidic acid acetyltransferase.  
DE  
XX Lysophosphatidic acid acetyltransferase; LPAAT; transgenic plant;  
KW triacylglycerol; oil content; ss.  
XX Triticum aestivum.  
XX  
FH Location/Qualifiers  
CDS  
FT 30..1154  
FT /\*tag= a  
FT /product= "lysophosphatidic acid acetyltransferase  
FT (LPAAT) isoenzyme"  
XX  
XX WO200049156-A2.  
PD 24-AUG-2000.  
XX 22-FEB-2000; 2000WO-US004526.  
XX 22-FEB-1999; 99US-0121119P.  
XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ, Ripp KG;  
XX WPI; 2000-558300/51.  
XX P-PSDB; AAB08479.  
XX  
XX New nucleic acid fragment encoding a lysophosphatidic acid  
PT acetyltransferase (LPAAT) isozyme, useful for creating transgenic plants  
PT which encode LPAAT at higher or lower levels than normal.  
XX  
XX Claim 39; Page 101; 102pp; English.  
XX  
XX The present sequence encodes a lysophosphatidic acid acetyltransferase  
CC (LPAAT) isoenzyme. The nucleic acid may be used to create transgenic  
CC plants which encode LPAAT at higher or lower levels than normal or in  
CC cell types or developmental stages in which they are not normally found.  
CC This would have the effect of altering the level of specific  
CC triacylglycerols in those cells, for e.g. overexpression of an LPAAT  
CC similar to the maize LPAAT will result in higher oil content in the seed,  
CC stem and leaf. LPAAT chimeric genes may be used for co-suppression of  
CC genes encoding LPAAT. The polynucleotides may also be used as probes for  
CC genetically and physically mapping the genes that are a part of, and as  
XX markers for traits linked to those genes  
SQ Sequence 1415 BP; 365 A; 299 C; 341 G; 410 T; 0 U; 0 Other;

QY 282 TTGTGGCTGAGCTTGTATGGCTTATTGATTGGTGGGAGGAGTTAAGTCCAAATATTC 341  
Db  
QY 329 CTGTGGCTCAGCTGGTCTGGCTTGTGGATTGGTGGGAGGAGTTAAGATACAACTGCAT 388  
Db  
QY 342 ACAGATCATGAACCTTTTCGTTTAATGGTAAAGAGCATGTCACCTTGTGATAAGCAATCAC 401  
Db  
QY 389 GCTGATGACGAACTTACAGGCAATGGGAATGAGCATGACCTTGTATATCAAAATAAT 448  
QY 402 AGAAGTGATATGATTGGCTTGTGGATTGGATTTTCAGCTCAGCGTTTCAGGTTGTCTTGGC 461  
Db  
QY 449 CGGAGCGATATCGATTGGCTTATTGGTGGATTGGTGGATTTGGCAGCGCTCAGGATGCCTTGA 508  
QY 462 AGCACTCTAGCTGTGATGAAGAAATCTTCAAAAGTTTCTGCCGGTCAATGGCTGGTCAATG 521  
Db  
QY 509 AGTACACTTGTGTTATGAAGAAATCATCGAAATTCCTTCCAGTTATTGGCTGGTCCATG 568  
QY 522 TGGTTTTCTGAGTATCTTTTCTGGAGAGAGTTGGCCAAAGGATGAAGACACATTAAG 581  
Db  
QY 569 TGGTTTGCAGATACTCTTTTGGAAAGGAGCTGGGCAAGGATGAAGACACATTGAA 628  
QY 582 TCAGGCATCCAGCGACTGAGTGATTTCCCTCTTCCCTTTGGCTAGCTCTCTTTGTAGAA 641  
Db  
QY 629 TGGGGCTCCAAAGGTTGAAGGACTTCCCGACCAATTTTGGCTAGCCCTTTTGTGAG 688  
QY 642 GGAACGCGTTTACACAGGCCAAACTATTAGCTGCTCAGGAATATGCCACTTCCACTGGA 701  
Db  
QY 689 GGCACCTCGCTTACTCCAGCAAGCTTCTAGCAGCTCAGGAGTATGCTGTTTCACAGGT 748  
QY 702 TTGCCTGTTCTAGAAATGTTTGTATCCAAAGAACTAAGGTTTGTCTTCTGAGTAACT 761  
Db  
QY 749 TTGCCAGCACCCAGAAATGATTGATTCCAGTACAAAGGATTTGTATCAGCTGTAAT 808  
QY 762 CATATGCGCTCAATTTGTTCTGCGCATTTATGATGAACAGTAGCCATCCCTAAGATTCC 821  
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QY 809 ATTATGCGGGATTTTGTCCAGCTATTATGATACAAACAGTAATTATCCAAAGATTCA 868  
QY 822 CCTGCTCCTAATGCTAAGACTCTTCAAGGACAACTTCAGTGGTGCATGTTTCATATC 881  
Db  
QY 869 CCTCAACCAACATGCTCGGATTTTGAAGGGCAATCTTCAGTGGTACATGTTTGGCATG 928  
QY 882 AAGAGGCATTTGATGAAGAACTGCCAGATACAGATGAGGCTGTTGCTCAATGGTGTGCGA 941  
Db  
QY 929 AAACGTCATGCAATGAGTGAGATGCCAAAGTCAGAAAGCAGATGTTTCAAAATGGTGCAA 988  
QY 942 GATATATTTGTGCGCAAGGATGCTTTGTTAGACAAACATATGGCTGAGGGTACTTTTAGT 1001  
Db  
QY 989 GACATCTTTGTAGCAAGGATGCAATTACTGGATAAGCATTTGGCGACAGGCACTTT--T 1045  
QY 1002 GATCAAGAGCTGAGGATACCTGGTCGACCAATAAAGTCTCTTCTGGTAGTTATATCTTGG 1061  
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QY 1046 GATGAGGATTAAGACCAATTGGCGCGCCAGTAAATCATTTGCTGGTACCTTGTGTTTGG 1105  
QY 1062 GCGTGTCTGTTGTTGCGGGTCTGTAAAGTTCTGCAATGCTTCTCGTTACTCTCTTCC 1121  
Db  
QY 1106 TCATGTCTCTTTTATATGGCGCGCTCAAGCTCTTCTATGGAATCACTCTGTCGACA 1165  
QY 1122 TGGAAGGGTGTGCAATTTTCAGCTTTTGGTTTGGCAGTTGTTTACTGCACCTATGCAAT 1181  
Db  
QY 1166 TGGAAGGAGTCGGGTTTACGGGCTTGGGCTGCACTGGTGGCGGCTCATGCAATGTC 1225  
QY 1182 CTGATTCAATTTCTCAGATCAGAGCGTTCAAACCGGCCAAG 1223  
Db  
QY 1226 TTTCATCATGTTCTCCAGTCAGAGCGATCGAGTCAGGCCAAG 1267

RESULT 9  
AAA64201  
ID AAA64201 standard; DNA; 1415 BP.  
XX  
AC AAA64201;  
XX  
DT 20-DEC-2000 (first entry)

QY 414 GATTGGCTTGTGGATGGTTTTCAGCTCAGCGTTTCAGGTTGTCTTGGCAGCACTCTAGCT 473  
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318 GATTGGCTGTTGGATGGATTATAGCACAGCGTTTCAGGATGTTCTTGAAGCGCAATAGCT 377  
QY 474 GTGATGAAGAAATCTTCAAAGTTTCTGCCGTCATTTGGCTGGTCAATGTGGTTTCTGAG 533  
Db |||||  
378 ATAATGAAGAAATCTCAAAGTTCTTCCAGTATTGGTTGGTCCATGGTTTGCAGAA 437  
QY 534 TATCTTTTCTCGAGAGAGTTGGGCCAAGGATGAAGCACATTAAGTCAGGCATCCAG 593  
Db |||||  
438 TACCTCTTTTTCGAGAGAGCTGGGCCAAGGATGAAGAAACACTTAATCGGTCCTTCAA 497  
QY 594 CGACTGAGTGATTTCCCTCTTCCCTTTTGGCTAGCTCTCTTTGTAGAGGAACGCGTTT 653  
Db |||||  
498 AGGTTGAAGACTTCCCGAGATCATTTTGGCTTGCCTTTTGTGAGGGTACAAGATT 557  
QY 654 ACACAGGCCAAACTATTAGCTGCTCAGGAATATGCCACTTCCACTGGATTGCTGTTCT 713  
Db |||||  
558 ACTCCAGCAAACTTTTAGCAGCTCAAGAAATATGCAGTCTCACAGGGTTGACAGCGCT 617  
QY 714 AGAAATGTTTGTATCCAAAGAACTAAGGTTTGTCTTCTGCAGTAAGTCATATCGGCTCA 773  
Db |||||  
618 AGGAATGTGCTGATTTCCACGAACAAAGGATTTGTATCAGCTGTAAATATTATGCGTGAC 677  
QY 774 TTTGTTCTGCTGCTTATGATGTAACAGTAGCCATCCCTAAGAGTTCCCTGCTCCTACA 833  
Db |||||  
678 TTTGTTCCAGTATCTACGATACAAAGTATTTCCGGAAGATTCCGCTAAACCAACA 737  
QY 834 ATGCTAAGACTCTTCAAGGACAACTTTCAGTGGTGCAATGTTTCATATCAAGAGGCAATTG 893  
Db |||||  
738 ATGCTGCGTATCTTTCAGGACAAATCATCAGTTGTTTCATGTCGCAATAAAACGCCATTCA 797  
QY 894 ATGAAGGAATGCTCCAGATACAGATGAGGCTTGTCTCAATGGTGTGAGATATATTGTG 953  
Db |||||  
798 ATGATGATATGCTTAATCGGATGAGGATGTTTCAAAATGGTGCAAGATATATTGTA 857  
QY 954 GCCAAGGATGCTTGTAGACAAACATATGGCTGAGGTAATTTTGTAGTCAAGAGCTG 1013  
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858 GCAAAGGACGCGTTATTGGACAAACATATAGCAACTGCTACTTT---TGATGAGGAAT 914  
QY 1014 CAGGATATGCTCGACCAATAAAGTCTCTTCTGGTAGTATATCTTGGGCGTGTCTGGTT 1073  
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915 ATACCAATGGCCGTCAGTGAAATCTTGTATGGTGTCTGCTGCTGCTGCTGCTGCTC 974  
QY 1074 GTTGGGGGCTGTAAAGTCTTCTGCAATGGTCTTCTGTAATCTCTTCTGGAAGGCTGTT 1133  
Db |||||  
975 CTATATGGTGTCTCATAGATTCTTACAGTGGAACCCAGCTCTTGTGCAAGGAGTG 1034  
QY 1134 GCATTTTTCAGCTTTTGGTTGGCAGTTGTTACTGCAATTTATGCAATTTCTGATCAATTC 1193  
Db |||||  
1035 ATCCTCTTGTCTTGTGATGGCAATGGTAACCGCGTTATGATGATTCATGATTCATGTTTC 1094  
QY 1194 TCACAGTCAGAGCGTTCAAACCCGGCCAA 1222  
Db |||||  
1095 TCGCAGGCGAGCGCTCAAGCTCTGCCAA 1123

RESULT 10

AAC50517

ID AAC50517 standard; DNA; 1391 BP.

XX

AC AAC50517;

XX

DT 18-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 65136.

XX

KW Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway; metabolic pathway;

KW promoter; termination sequence; ss.

XX

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-00301439.  
XX  
PR 25-FEB-1999; 99US-0121825P.  
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Qy	448	CAGTTGTCTTGGCAGCACTCTAGCTGTGATGAAGAAATCTTCAAAGTTTCTGCCGGTCA	507
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Qy	808	TCCTAAGAGTTTCCCCTGCTCTCTACAAATGCTAAGACTCTTTCAAGGGACAACCTTCACTGG	867
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QY	1108	CGTTACTCTCTTCCCTGGAAAGGTGTTGCATTTTTCAGCTTTTGGTTTGGCAGTTGTTACTG	1167
Db	1068	AGCTCCTATCGACATGGAGAGGAGTGGCATTCACTGCCGACGGATGGCGCTCGTGACAG	1127
QY	1168	CACTTATGCAAAATTCGATTCAAATTCACAGTCAGAGCGTTTCAAAACCGGCCCAAG	1223
Db	1128	GGGTCAATGACCGTCTTCGTCATGTTCTCCAGGCTGAGCGATCGAGCTCAGGCCAAG	1183

## RESULT 14

RESOL 14  
AAA64184  
ID AAA64184 standard; DNA: 570 BP.

AC AAA64184:

DT 20-DEC-2000 (first entry)

DE Nucleotide sequence of a lysophosphatidic acid acetyltransferase.

KW Lysophosphatidic acid acetyltransferase; LPAAT; transgenic plant  
KW triacylglycerol; oil content; ss.

OS  
Triticum aestivum.

XX	Key	Loc
FH		

CD5  
22. .502  
/\* Lag= a

FT lysophosphatidic acid acetyltransferase  
/product= "lysophosphatidic acid acetyltransferase"  
(LPAAT) isoenzyme"  
FT

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FI "no termination codon given
XX
XX
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PN WC200045156-A2.  
XX

PD 24-AUG-2000.  
XX

PF 22-FEB-2000; 2000WO-US004526.  
XX

PR 22-FEB-1999;  
YY

PA (DUPO) DU E  
XX

PI Cahoon EB, Cahoon RE, Hitz WD, Kiny  
yy

DR WPI; 2000-558300/51.  
DR P-PCPB. XAP08462

DE  
XX

acetyltransferase (LPAAT) isozyme, useful for creating

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CC (LPAAT) isoenzyme. The nucleic acid may be used to create transgenic

CC cell types or developmental stages in which they are not normally found.



PR	16-JUL-1999;	99US-0144086P.	PR	08-OCT-1999;	99US-0158232P.
PR	19-JUL-1999;	99US-0144325P.	PR	12-OCT-1999;	99US-0158369P.
PR	19-JUL-1999;	99US-0144331P.	PR	13-OCT-1999;	99US-0159293P.
PR	19-JUL-1999;	99US-0144332P.	PR	13-OCT-1999;	99US-0159294P.
PR	19-JUL-1999;	99US-0144333P.	PR	13-OCT-1999;	99US-0159295P.
PR	19-JUL-1999;	99US-0144334P.	PR	14-OCT-1999;	99US-0159329P.
PR	19-JUL-1999;	99US-0144335P.	PR	14-OCT-1999;	99US-0159330P.
PR	20-JUL-1999;	99US-0144352P.	PR	14-OCT-1999;	99US-0159331P.
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PR	12-AUG-1999;	99US-0148341P.			
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PR	20-AUG-1999;	99US-0149722P.			
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PR	23-AUG-1999;	99US-0149930P.			
PR	25-AUG-1999;	99US-0150566P.			
PR	26-AUG-1999;	99US-0150884P.			
PR	27-AUG-1999;	99US-0151065P.			
PR	27-AUG-1999;	99US-0151066P.			
PR	27-AUG-1999;	99US-0151080P.			
PR	30-AUG-1999;	99US-0151303P.			
PR	31-AUG-1999;	99US-0151438P.			
PR	01-SEP-1999;	99US-0151930P.			
PR	07-SEP-1999;	99US-0152363P.			
PR	10-SEP-1999;	99US-0153070P.			
PR	13-SEP-1999;	99US-0153758P.			
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PR	20-SEP-1999;	99US-0154779P.			
PR	22-SEP-1999;	99US-0155139P.			
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PR	07-OCT-1999;	99US-0158232P.			

Query Match

Best Local Similarity

Mismatches

Conservative

Score

210.8;

DB

3;

Length

485;

Pred. No.

8.4e-45;

QY	330	GTCCAATATTACAGATCATGAAACCTTTCGTTTAATGGTAAAGAGCATGCACCTGTG	389
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QY	450	GGTTGCTTGGCAGCACTCTAGCTGTGATGAAGAAATCTTCAAAGTTTCGCCGTCA	509
Db	279	GGTGCCTTGAAGTACGCTCGTGTATGAAGAAAGTCACTCAAGTTCTTCCAGTCATT	338
QY	510	GGCTGGTCAATGTGGTTTCTGAGTATCTTTTCTGGAGAGAAAGTTGGCCCAAGATGAA	569
Db	339	GGCTGGTCAATGTGGTTTGCAGAGTACCTCTTTTGGAGAGGAGCTGGCCCAAGATGAA	398
QY	570	AGCACATTAAGTCAGGCATCCAGGCAGTGAATTCCTCTTCCCTTTTGGGTAGCT	629
Db	399	AAGACATAAAGTGGGGTCTCCAAAGGTTGAAGACTTCCCTAGACCATTTTGGGTAGCT	458
QY	630	CTCTTTGTAGAAGGACGCGTTTTCAC	655
Db	459	CTTTTGTGAGGGTACTCGCTTTAC	484

Search completed: July 9, 2004, 19:52:37

Job time : 472 secs







QY 404 AAGTGATATTGATTGGCTTGTGGATGGTTTCAGCTCAGCGTTTCAGGTTGTCTTGGCAG 463  
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QY 408 GAGTGATATTGATTGGCTCATGATGGATATTGGCCAGCGTTTCAGGTTGCCTTGGAG 467  
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QY 464 CACTCTAGCTGTGATGAAGAAATCTTCAAAGTTTCTGCCGGTCATTGGTGGTCAATGTG 523  
Db |||||  
QY 468 TACACTTGTCTCATGAAGAAGTCATCCAAGTTCCTTCCAGTTATTGGTGGTCAATGTG 527  
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QY 524 GTTTTCTGAGTATCTTTTCTGGAGAGAAGTTGGGCCAAGGATGAAGACACATTAAAGTC 583  
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QY 528 GTTTGCAGAGTACCTCTTTTGGAAAGGAGCTGGGCCAAGGATGAAGACACATAAGTG 587  
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QY 584 AGGCATCCAGCGACTGAGTGATTTCCCTCTCCCTTTTGGCTAGCTCTCTTTGTAGAAGG 643  
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QY 588 GGGTCTCCAAAGGTTGAAAGACTTCCCTAGACCATTTTGGCTAGCTCTTTTCGTCGAGGG 647  
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QY 644 AACGCGTTTACACAGGCCAAACTATTAGCTGCTCAGGAATATGCCACTTCCACTGGATT 703  
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QY 648 TACTCGCTTACTCCAGCAAGCTTCTCGCAGCTCAGGAATATCGCGCTCCAGGGCTT 707  
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QY 704 GCCTGTTCTAGAAATGTTTGTATTCCAAAGAACTAAGGTTTGTCTTCTGCAGTAAGTCA 763  
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QY 708 ACCGGCTCTAGAAATGTACTATTCCACGTACCAAGGATTTGTATCTGCTGTAAGTAT 767  
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QY 764 TATGCGTCAATTTGTTTCTGCTGCTTCAAGGCAACCTTTCAGTGGTGATGTTTCAATCAA 883  
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QY 824 TGCTCTACAAATGCTAAGACTCTTCAAGGCAACCTTTCAGTGGTGATGTTTCAATCAA 883  
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QY 884 GAGGCATTTGATGAAGAACTGCCAGATACAGATGAGGCTGTTGCTCAATGGTGTCGAGA 943  
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QY 948 CATTTTGTGGCAAGGATGCTTTACTGGAACAGCATTTGGCAACAGGCACTTT---CGA 1004  
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QY 1004 TCAAGAGCTGAGGATACCTGTCGACCAATAAAGTCTCTTCTGGTAGTTATATCTTGGGC 1063  
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QY 1005 TGAGGAGATTAGACCTATTGGCGCTCCAGTGAATCATTTGCTGGTGACCCCTGTTCTGTC 1064  
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QY 1064 GTGCTGTTGTTGCGGGTCTGTAAAGTTCTGCTGCAATGGTCTTCTGTTACTCTCTCTG 1123  
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QY 1065 GTGCTCTCTGCTGTTTGGCGCATCGAGTTCTCAAGTGGACACAGCTTCTGTCGACGTG 1124  
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QY 1124 GAAGGGTGTGCAATTTTCAAGCTTTTGGTTGGCAGTTGTTTACTGCACTTATGCAAAATCT 1183  
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QY 1184 GATTCAATTTCAAGTCAGAGCGTTCAAACCCGGCCAAG 1223  
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QY 1185 CATCATGTTCTCCAGGCTGAGCGGTGAGCTCAGCTCAGCCAGG 1224  
Db |||||

RESULT 3  
US-08-941-319-1  
; Sequence 1, Application US/08941319  
; Patent No. 5945323  
; GENERAL INFORMATION:  
; APPLICANT: SLABAS, ANTONI R.  
; APPLICANT: BROWN, ADRIAN P.  
; TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: US  
; ZIP: 20005-3934

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/941,319  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/454,267  
FILING DATE: 08-JUN-1995  
APPLICATION NUMBER: PCT/GB93/02528  
FILING DATE: 10-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: REED, GRANT E.  
REGISTRATION NUMBER: P-41,264  
REFERENCE/DOCKET NUMBER: 0623.0310000/JAG/GER  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1514 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 130..1254  
US-08-941-319-1

Query Match 36.6%; Score 548.8; DB 2; Length 1514;  
Best Local Similarity 68.8%; Pred. No. 3.1e-158;  
Matches 770; Conservative 0; Mismatches 347; Indels 3; Gaps 1;

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QY 108 GCGGCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 167  
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QY 164 CCTGCTCTTCTTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCT 223  
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QY 224 CGTAAGCGCGGTGTCGAAAAGTTTGTACAGAAAGATCAACCGGGTAGTAGCAGAGCTCT 283  
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QY 228 GATAAGGCGCTTTTCGAAGAGCTTCTACCGTCGATCAACAGATTTCTTGGCCGAGCTGT 287  
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QY 288 GTGGCTTCACTTGTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 347  
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QY 404 AAGTCATATTGATTGGCTTGTGGATGGGTTTTCAGCTCAGCGTTTCAGGTTGTCTTGGC 463  
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QY 464 CACTCTAGCTGTGATGAAGAAATCTTCAAAGTTTCTCCGGTCATTGGCTGGTCAATGTG 523  
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Db |||||

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QY	704	GCTGT	TCCTAGAAATGTTTTTGATTTCCAAGAACTAAGGGTTTGTCTTCTGCAGTAAGTCA	763	
Db	708	ACGGCT	CCTAGAAATGTACTTATTTCCACGTACCAAGGATTGTATCTGCTGTAAGTAT	767	
QY	764	TATGCGCT	CAITTTGTTTCTTGCCATTTATGATGTAAACAGTAGCCATCCCTAAGAGTTCCCC	823	
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QY	884	GAGGCAT	TTTGATGAAGGAACTGCCAGATACAGATGAGGCTGTGTCTCAATGGTGTTCGAGA	943	
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QY	944	TATAT	TTGTGGCCAAAGGATGCTTTTGTTAGACAAACATATGGCTGAGGGTACTTTTAGTGA	1003	
Db	948	CAT	TTTTTGTGGCAAAGGATGCTTACTTGGACAAAGCATTTGGCAACAGGCACCTTT--CGA	1004	
QY	1004	TCAA	GAGCTGCAGGATACTGGTCGACCAATAAAGTCTCTTCTGGTAGTTATATCTTGGGC	1063	
Db	1005	TGAG	GAGATTAGACCTATTGGCGGTCAGTGTAAATCATTGTGTGTGACCCGTCTCTGGTC	1064	
QY	1064	GTGT	CTGTGTTGTGGGGGTCTGTAAAGTTCCTGCAATGGTCTTCGTTACTCTTCTCCTG	1123	
Db	1065	GTG	CTCCTGTGTTTGGCGCCATCGAGTTCTTCAAGTGGACACAGCTTCTGTGACCGTG	1124	
QY	1124	GAAG	GGTGTGTCATTTTTCAGCTTTTGGTTTGGCAGTTGTTTACTGCACTTATGCAAAATCT	1183	
Db	1125	GAG	GGTGTGGCGTTTCACTGCGCGCAGGGATGGCGCTTGTGACGGGTGTCTATGTCATGTCTT	1184	
QY	1184	GATT	CAATTTCTCACAGTCAAGCGGTTCAAAACCGGCCAAG	1223	
Db	1185	CAT	CATGTTCTCCAGGCTGACGGGTGAGCTCAGCCAGG	1224	

## RESULT 4

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US-09-035-098-1
; Sequence 1, Application US/09035098
; Patent No. 6194640
; GENERAL INFORMATION:
; APPLICANT: SLABAS, ANTONI R.
; APPLICANT: BROWN, ADRIAN P.
; TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,098
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/454,267
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: REED, GRANT E.
; REGISTRATION NUMBER: P-41,264
; REFERENCE/DOCKET NUMBER: 0623-0310000/JAG/GER

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Db 888 ACGTCATGCAATGAGTGAGATGCCAAATCAGATGAGGATGTTTCAAAATGGTGTAAAGA 947  
QY 944 TATATTTGGCCCAAGGATGCTTTTGTAGACAAACATATGGCTGAGGGTACTTTTAGTGA 1003  
Db 948 CATTTTGTGGCAAGGATGCTTACTGGACAAGCATTTGGCAACAGGCACCTTT---CGA 1004  
QY 1004 TCAAGAGTGCAGGATACTGGTCGACCAATAAAGTCTCTTCTGGTAGTTATATCTTGGGC 1063  
Db 1005 TGAGGAGATAGACCTATTGGCCGTCAGTGAATCATTTGCTGGTGACCCCTGTTCTGGTC 1064  
QY 1064 GTGCTGCTGTTTGGGGCTCTGTAAAGTCTCTGCAATGGTCTTCTGTTACTCTCTTCTCTG 1123  
Db 1065 GTGCCCTCCTGCTGTTTGGCGCCATCGAGTCTTCAAGTGGACACAGCTTCTGTGCGAGTG 1124  
QY 1124 GAAGGGTGTGCTATTTTCAGCTTTTGGTGTGGCAGTTGTTACTGCACTTATGCAATTTCT 1183  
Db 1125 GAGGGGTGTGGCGTTCACTGCCGACAGGATGGCGCTTGTGACGGGTGTGATGCAATGCTT 1184  
QY 1184 GATTCAATTTCTACAGTCAGAGCGTTTCAAAACCCGGCCAAAG 1223  
Db 1185 CATCATGTTCTCCAGGCTGAGCGGTGAGCTCAGCCAGG 1224

RESULT 5  
US-09-215-252-12  
; Sequence 12, Application US/09215252  
; Patent No. 6300487  
; GENERAL INFORMATION:  
; APPLICANT: LEUNG, David W.  
; APPLICANT: ADOUREL, Daniel  
; APPLICANT: HOLLENBACK, David  
; TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE  
; FILE REFERENCE: 077319/0151  
; CURRENT APPLICATION NUMBER: US/09/215,252  
; CURRENT FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: US 08/618,651  
; PRIOR FILING DATE: 1996-03-19  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 1660  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (184)..(1311)  
US-09-215-252-12

Query Match 8.1%; Score 121.8; DB 4; Length 1660;  
Best Local Similarity 46.9%; Pred. No. 6.5e-27;  
Matches 415; Conservative 0; Mismatches 467; Indels 3; Gaps 1;  
QY 146 CGTGGTGATACCATTTGGGCTGCTCTTCTTCGCCCTCCGGCTCCTTTAATCTCATCA 205  
Db 216 CGTGTGCACCTGCTGGTCTGCTTGTCTCGTGGTGAGTGGTCTGGTCATCACTTCGT 275  
QY 206 GGCAATATGCTATGCTGTAAGGCGGTGTCGAAAAGTTGTACAGAAGGATCAACCG 265  
Db 276 CCAGCTGTGCACGCTGGCGCTCTGGCCGTCAGCAAGCAGCTCTACCGCCGCTCAACTG 335  
QY 266 GGTAGTAGCAGAGCTCTTGTGGCTGGAGCTGTATGGCTTATTGATTGGTGGGCAGGAGT 325  
Db 336 CCGCCTCGCATACTCACTCTGGAGCCAACTGGTCACTGCTGGAGTGGTGGTCTCTGCAC 395  
QY 326 TAAGGTCCAAATATTCACAGATCATGAACCTTTCTGTTTAAATGGGTAAGAGCATGCACT 385  
Db 396 GGAGTGTAATGTTTACGGACAGGCCACGGTAGAGCGCTTTGGGAAGGAGCAGCGAGT 455  
QY 386 TGTGATAAGCAATCACAGAAGTATATTGATTGGCTTGTGATGGTGTTCAGCTCAGCG 445  
Db 456 CATCATCTCAACCAACAACTTCGAGATCGACTTCTCTGTGGTGGACCATGTGTGAGCG 515  
QY 446 TTCAGGTTGCTTGGCAGCACTCTAGCTGTGATGAAGAAATCTTCAAGTTTCTGCCGCT 505

Db 516 CTTGGAGTGTGGGAGCTCAAGGTCTCGCTAAGAGGAGCTGCTTACGTGCCCT 575  
QY 506 CATTGGCTGCTCAATGTGTTTCTGAGTATCTTTTCTGAGAGAAAGTTGGGCCAAGGA 565  
Db 576 CATCGGCTGGACGTGTACTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGGA 635  
QY 566 TGAAGACATTAAGTCAAGCATCCAGCATCCAGCACTAGTGAATTCCTCTTCCCTTTTGGCT 625  
Db 636 CCGGACACCGTGGTGAAGGGCTGAGGCGCTGTCCGACTACCCCGAGTACATGTGTT 695  
QY 626 AGCTCTCTTTGTAGAAAGAACCGCTTTTACACAGGCCAAACTATTAGCTGCTCAGGAATA 685  
Db 696 TCTCTGTACTGCGAGGGGACCGCTTACGGAGACCAAGCACCGCGTTAGCATGGAGGT 755  
QY 686 TGCCACTTCCACTGGATTGCTGCTGTTCTAGAAATGTTTGTATTTCAAGAACTAAGGTTT 745  
Db 756 GCGGCTGCTAAGGGCTTCTGCTCTCAAGTACCACTGCTCCCGGACCAAGGCTT 815  
QY 746 TGTTTCTGCAGTAAGTCATATGCGCTCATTTGTTCTGCTGCCATTTATGATGAACAGTAGC 805  
Db 816 CACCACCGCAGTCAAGTGCCTCCGGGGGACAGTCGCAGCTGTCTATGATGAACCTTGA 875  
QY 806 CATCCCTAAGAGTTCCCTCTCTACAATGCTAAGACTCTTCAAGGGACAACTTTCAGT 865  
Db 876 CTTT---AGAGAAACAAGAACCCGTCCTCTGCTGGGATCCTCTACGGGAAGATACGA 932  
QY 866 GGTGCATGTTTCATATCAAGAGGCATTTGATGAAGAACTGCTCCAGATACAGATGAGGCTGT 925  
Db 933 GCGGACATGTGCTGAGGAGATTTCTCTGGAAGACATCCCGCTGGATGATAAAGGAAGC 992  
QY 926 TGCTCAATGTTGTCGAGATATATTTGTGCCAAAGGATGCTTTGTTAGACAAACATATGC 985  
Db 993 AGCTCAGTGGCTTCATAACTGTACCAAGGAGGACGCGCTCCAGGAGATATATAATCA 1052  
QY 986 TGAGGGTACTTTTAGTGATCAAGAGCTGCAGGATACCTGTCGACC 1030  
Db 1053 GAAGGCGATGTTTCCAGGGGAGCAGTTTAAGCTGCCCGGAGGCC 1097

RESULT 6  
US-09-970-989A-12  
; Sequence 12, Application US/09970989A  
; Patent No. 6670143  
; GENERAL INFORMATION:  
; APPLICANT: LEUNG, DAVID W.  
; APPLICANT: ADOUREL, DANIEL  
; APPLICANT: HOLLENBACK, DAVID  
; TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE  
; FILE REFERENCE: 077319/0275  
; CURRENT APPLICATION NUMBER: US/09/970,989A  
; CURRENT FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: 09/215,252  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 08/618,651  
; PRIOR FILING DATE: 1996-03-19  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 1660  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (184)..(1311)  
US-09-970-989A-12

Query Match 8.1%; Score 121.8; DB 4; Length 1660;  
Best Local Similarity 46.9%; Pred. No. 6.5e-27;  
Matches 415; Conservative 0; Mismatches 467; Indels 3; Gaps 1;  
QY 146 CGTGGTGATACCATTTGGGCTGCTCTTCTTCGCCCTCCGGCTCCTTTAATCTCATCA 205



Db 216 CGTGTGCACCTGCTGGTGGCTTTGTCTCGTGGTGGTGGTCTGCTCATCAACTTCGT 275  
Qy 206 GGCAATATGCTATGTCGTAAAGCGCGTGTGCGAAAGTTTGTACAGAGGATCAACCG 265  
Db 276 CCAGCTGTGCACGCTGGCGCTCTGGCGGTGAGCAAGCAGCTCTACCGCGCTCAACTG 335  
Qy 266 GGTAGTAGCAGAGCTCTTGTGGCTGGAGCTGTATGGCTTATTGTTGGTGGCAGGAGT 325  
Db 336 CCGCTCGCATACTACTCTGGAGCCAACTGGTCACTGCTGGAGTGGTGGTCTGTCAC 395  
Qy 326 TAAGTCCAAATATTACAGATCATGAACCTTTCGTTTAATGGTAAAGAGCATGCACT 385  
Db 396 GGAGGTACACTGTTACCGGACCAGGCCAGGTAGAGCGCTTTGGGAAGGAGCAGCAGT 455  
Qy 386 TGTGATAAGCAATACAGAAAGTGATATTGATGGCTTGTGGATGGGTTTTCAGCTCAGCG 445  
Db 456 CATCATCTCAACCAACTTTCGAGATCGACTTCTCTGTGGTGGACCATGTGTGAGCG 515  
Qy 446 TTCAGGTGTCTTGGCAGCACTCTAGCTGTGATGAAGAAATCTTCAAGTTTTCGCCGGT 505  
Db 516 CTTGGAGTGTGGGAGCTCCAAAGTCTCGTAAAGAGGAGTGTCTACGTGCCCT 575  
Qy 506 CATTGGCTGGTCAATGTGGTTTCTGAGTATCTTTTCTGGAGAAAGTTGGGCAAGGA 565  
Db 576 CATCGGCTGGACGTGTTACTTCTGAGATTTGTCTGCAAGCGAAGTGGGAGGAGGA 635  
Qy 566 TGAAAGCACATTAAGTCAGGCATCCAGGCATCCAGGCATGAGTATTTCCCTCTTCCCTTTGGCT 625  
Db 636 CCGGACACCGTGGTGAAGGCTGAGCGCTGTGCGACTACCCGAGTACATGTGTT 695  
Qy 626 AGCTCTCTTGTAGAGAAACGGTTTACACAGGCCAACTATTAGCTGTCTCAGGAATA 685  
Db 696 TCTCTGTACTGCGAGGGGACGGCTTACGGAGAACCAAGCACCGGCTTAGCATGGAGGT 755  
Qy 686 TGCCACTTCCACTGGATGCTCTTCTAGAAATGTTTGTATCCAAAGAACTAAGGGTTT 745  
Db 756 GGCGGTGCTAAGGGCTTCTGTCTCAAGTACCACTGCTGCGCGGACCAAGGGCTT 815  
Qy 746 TGTTTCTGCAGTAAGTCATATCGCTCATTTGTTCTCTGCCATTTATGATGTAACAGTAGC 805  
Db 816 CACCACCGCAGTCAAGTGCCTCCGGGGACAGTCCGAGCTGTCTATGATGTAACCTGAA 875  
Qy 806 CATCCCTAAGAGTTCCTCTGCTTACATGCTAAGACTCTTCAAGGACCAACCTTCAGT 865  
Db 876 CTTC---AGAGGAACAAGAACCCGTCCTGCTGGGATCCTCTACGGGAAGAGTACGA 932  
Qy 866 GGTGATGTTTCATATCAAGAGGCAATTTGATGAAGAACTCCAGATACAGATGAGGCTGT 925  
Db 933 GGCGGACATGTGCGTGGAGGATTTCTCTCTGGAAGACATCCCGTGGATGAAAGGAAGC 992  
Qy 926 TGCTCAATGGTGTGAGATATATTGTGGCCAAAGGATGCTTTTGTAGACAAACATATGGC 985  
Db 993 AGCTAGTGGCTTTCATAAAGTGTACAGGAGAAAGGACGCGCTCCAGGAGATATATATCA 1052  
Qy 986 TGAGGTACTTTTACTGATCAAGAGCTGCAGGATGCTGGTGGCACC 1030  
Db 1053 GAAGGACATGTTTCCAGGGGAGCAGTTTAAGCCTGCCCGGAGGCC 1097

RESULT 7

US-09-620-312D-841  
; Sequence 841, Application US/09620312D  
; Patent No. 6569662

; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chonghua  
; APPLICANT: Asundi, Vinod

; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyan

; APPLICANT: Chen, Rui-hong  
; APPLICANT: Zhao, Qing A.

; APPLICANT: Wehrman, Tom  
; APPLICANT: Xue, Aidong J.

; APPLICANT: Yang, Yonghong  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Zhou, Ping  
; APPLICANT: Ma, Yunding  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: John Tillinghast  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and  
; FILE REFERENCE: 784CIP2B  
; CURRENT APPLICATION NUMBER: US/09/620,312D  
; CURRENT FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 1105  
; SOFTWARE: pt\_FL\_genes Version 1.0  
; SEQ ID NO 841  
; LENGTH: 1769  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (211)..(1272)  
US-09-620-312D-841

Query Match 8.0%; Score 120.2; DB 4; Length 1769;  
Best Local Similarity 46.8%; Pred. No. 2.1e-26;

Matches 414; Conservative 0; Mismatches 468; Indels 3; Gaps 1;

Qy 146 CGTGTGGTACCATTTGGCGCTGCTCTTCTTCCGCTCCGCGCTCCTTGTAAATCTCATCA 205  
Db 243 CGTGTGCACCTGCTGGTGGCTTGTCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 302  
Qy 206 GGCAATATGCTATGTCGTGTAAGCGCGGTGTGCAAAAGTTTGTACAGAGGATCAACCG 265  
Db 303 CCAGCTGTGCACGCTGGCGCTCTGGCGGTGAGCAAGCAGCTCTACCGCGCTCAACTG 362  
Qy 266 GGTAGTAGCAGAGCTTGTGGCTGGAGCTTGTATGGCTTATGATGGTGGGAGGAGT 325  
Db 363 CCGCTTGGCTTCTCACTCTGGAGCAACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 422  
Qy 326 TAAGTCCAAATATTACAGATCATGAACCTTTCGTTTAAATGGGTAAGAGATGCACT 385  
Db 423 GGAGGTACACTGTTACGGACCGGACCGGACCGGACCGGACCGGACCGGACCGGACCG 482  
Qy 386 TGTGATAAGCAATACAGAGAGTATGATTTGATTTGGCTTGTGGATGGGTTTTCAGTCA 445  
Db 483 CATCATCTCAACCAACTTTCGAGATCGACTTCTCTGTGGTGGACCATGTGTGAGCG 542  
Qy 446 TTCAGGTGTCTTGGCAGCACTCTAGCTGTGATGAAGAAATCTTCAAGTTTCTGCCGGT 505  
Db 543 CTTGGAGTGTGGGAGCTCCAGGTCCTCGTAAAGAGGAGTGTCTCTACGTGCCCT 602  
Qy 506 CATTGGCTGGTCAATGTGGTTTCTGAGTATCTTTTCTGGAGAGAGTTGGGCAAGGA 565  
Db 603 CATCGGCTGGAGCTGTTCTTCTGGAGATTGTGTTCTGCAAGGAGGAGTGGGAGGAGGA 662  
Qy 566 TGAAGACACATTAAGTCAAGGCTCAGGATCCAGGCTGAGTATTTCCCTCTTCCCTTTGGCT 625  
Db 663 CCGGACACCGTGGTCAAGGGCTGAGGCGCTGTGCGACTACCCGAGTACATGTGTT 722  
Qy 626 AGCTCTCTTGTAGAGGAAACGGTTTACACAGGCCAACTATTAGCTGTCTCAGGAATA 685  
Db 723 TCTCTGTACTGCGAGGGGACGGCTTTCAGGAGACCAAGCAGCGCTTAGCATGGAGGT 782  
Qy 686 TGCCACTTCCACTGGATGCTGTCTTCTAGAAATGTTTGTAGTTCCAAAGAACTAAGGGTTT 745  
Db 783 GGCGGTGCTAAGGGCTTCTCTGTCTCAAGTACCACTGCTGCGCGGACCAAGGGCTT 842  
Qy 746 TGTTTCTGCAGTAAGTCAATGCTGCTCATTTGTTCTGCTGCTGCTGCTGCTGCTGCTGCT 805

Db 843 CACCACCGCAGTCAAGTCCCTCGGGGGACAGTCGCAGCTGTCTATGATGTAACCCCTGAA 902  
QY 806 CATCCCTAAGAGTCCCTGCTCCTACAAATGCTAAGACTCTTCAAGGGACAACCTTTCAGT 865  
Db 903 CTTTCC--AGAGGAAACAAGAACCCGTCCTGCTGGGATCTCTACGGGAAGATACGA 959  
QY 866 GGTGCATGTTTCATATCAAGAGGCATTTGATGAAGGAACCTGCCAGATACAGATGAGGCTGT 925  
Db 960 GCGGACATGTGCGTGAGGAGATTTCTCTGGAAGACATCCCGCTGGATGAAAGGAAGC 1019  
QY 926 TGCTCAATGTTGTCGAGATATATTTGTGGCAAGGATGCTTTGTTAGACAAAACATATGCC 985  
Db 1020 AGCTCAGTGGCTTCATAAAGTACCAAGGAGGACGCGCTCCAGGAGATATATAATCA 1079  
QY 986 TGAGGGTACTTTTAGTGATCAAGAGCTGCAGGATACTGTGTCGACC 1030  
Db 1080 GAAGGGCATGTTTCCAGGGGAGCAGTTTAAAGCTGCCCGGAGGCC 1124

RESULT 8  
US-09-215-252-14  
; Sequence 14, Application US/09215252  
; Patent No. 6300487  
; GENERAL INFORMATION:  
; APPLICANT: LEUNG, David W.  
; APPLICANT: ADOUREL, Daniel  
; APPLICANT: HOLLENBACK, David  
; TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE  
; FILE REFERENCE: 077319/0151  
; CURRENT APPLICATION NUMBER: US/09/215,252  
; CURRENT FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: US 08/618,651  
; PRIOR FILING DATE: 1996-03-19  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 1523  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (233)..(1174)  
US-09-215-252-14

Query Match 7.2%; Score 108.6; DB 4; Length 1523;  
Best Local Similarity 47.6%; Pred. No. 7e-23;  
Matches 352; Conservative 0; Mismatches 384; Indels 3; Gaps 1;

QY 292 AGCTTGATGGCTTATTGATGGTGGGACGAGTTAAGTCCAAATATTCACAGATCATG 351  
Db 225 AACTGGTCATGCTGCTGGAGTGGTGGTCTGACGGAGGTGTACACTGTTACGGACCAGG 284  
QY 352 AAACCTTTTCGTTTAATGGGTAAGAGCATGCACTTGTGATAAGCAATCACAGAAAGTGATA 411  
Db 285 CCACGGTAGACCGCTTTGGGAAGGAGCACGAGTCATCATCTCAACCAACTTCGAGA 344  
QY 412 TTGATTGGCTTGTGGATGGGTTTCAGCTCAGCGTTTCAGGTGTCTTGGCAGCACTCTAG 471  
Db 345 TCGACTTCTCTGTGGGTGGACCATGTGTGAGCGCTTCGGAGTGTCTGGGAGCTCCAGG 404  
QY 472 CTGTGATGAAGAAATCTTCAAAGTTTCTCCCGGTCAATTGGCTGGTCAATGTGTTTCTG 531  
Db 405 TCCTCGCTAAGAAGGAGCTGCTCTACGTGCCCTCATCGCTGGACGTGGTACTTTCTGG 464  
QY 532 AGTATCTTTTCTGGAGAGAGTGGGCCAAGGATGAAGCACATTAAAGTCAGGCATCC 591  
Db 465 AGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGCACCGTGCTGAAGGGCTGA 524  
QY 592 AGCGACTGAGTGATTTCCCTCTTCCCTTTTGGCTAGCTCTCTTTGTAGAAGGAACGCGTT 651  
Db 525 GCGCCTGTGCGACTACCCCGAGTACATGTGTTTCTCTGTACTGCGAGGGGACGCGCT 584

QY 652 TTACACAGGCCAACTATTAGCTGCTCAGGAATATGCCACTTCCACTGGAATGCTGCTTTC 711  
Db 585 TCACGGAGACCAAGCACCCGCTTAGCATGGAGTGGCGGCTGTGAAGGGGCTTCTCTGTCC 644  
QY 712 CTAGAAATGTTTTGATTCCAAGAACTAAGGTTTTTGTCTGAGTAAGTCATATGCGCT 771  
Db 645 TCAAGTACCACCTGCTGCCGGACCAAGGGCTTCAACCAGCGAGTCAAGTGCCTCCGG 704  
QY 772 CATTTGTTCTGCCATTTATGATGTAAACAGTAGCCATCCCTAAGAGTTCCTCTGCTCCTA 831  
Db 705 GGACAGTCGAGCTGTCTATGATGTAAACCTGAACCTTC--AGAGGAAACAAGAACCCGT 761  
QY 832 CAATGCTAAGACTCTTCAAGGGACAACCTTCAAGTGGTGCATGTTTCATATCAAGAGGCATT 891  
Db 762 CCTGCTGGGATCTCTACGGGAAGAAGTACGAGCGGACATGTGCGTGGAGAGATTTC 821  
QY 892 TGATGAAGGAACCTGCCAGATACAGATGAGGCTGTGTTGTTCAATGGTGTGAGATATATTG 951  
Db 822 CTCTGGAAGACATCCCGCTGGATGAAAAGGAAGCAGCTCAGTGGCTTCATAAACTGTACC 881  
QY 952 TGGCCAAGGATGCTTTGTTAGACAAACATATCGCTGAGGGTACTTTTAGTGATCAAGAGC 1011  
Db 882 AGGAGAAGGACGCGCTCCAGGAGATATATATCAGAAGGGCATGTTTCCAGGGGAGCAGT 941  
QY 1012 TGCAGGATACTGTGTCGACC 1030  
Db 942 TTAAGCCTGCCCGGAGGCC 960

RESULT 9  
US-09-970-989A-14  
; Sequence 14, Application US/09970989A  
; Patent No. 6670143  
; GENERAL INFORMATION:  
; APPLICANT: LEUNG, David W.  
; APPLICANT: ADOUREL, DANIEL  
; APPLICANT: HOLLENBACK, DAVID  
; TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE  
; FILE REFERENCE: 077319/0275  
; CURRENT APPLICATION NUMBER: US/09/970,989A  
; CURRENT FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: 09/215,252  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 08/618,651  
; PRIOR FILING DATE: 1996-03-19  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 1523  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (233)..(1174)  
US-09-970-989A-14

Query Match 7.2%; Score 108.6; DB 4; Length 1523;  
Best Local Similarity 47.6%; Pred. No. 7e-23;  
Matches 352; Conservative 0; Mismatches 384; Indels 3; Gaps 1;

QY 292 AGCTTGATGGCTTATTGATGGTGGGACGAGTTAAGTCCAAATATTCACAGATCATG 351  
Db 225 AACTGGTCATGCTGCTGGAGTGGTGGTCTGACGGAGGTGTACACTGTTTACGGACCAGG 284  
QY 352 AAACCTTTTCGTTTAATGGGTAAGAGCATGCACTTGTGATAAGCAATCACAGAAAGTGATA 411  
Db 285 CCACGGTAGAGCGCTTTGGGAAGGAGCACGAGTCATCATCTCAACCAACTTCGAGA 344  
QY 412 TTGATTGGCTTGTGGATGGGTTTCAGCTCAGCGTTTCAGGTGTCTTGGCAGCACTCTAG 471  
Db 345 TCGACTTCTCTGTGGGTGGACCATGTGTGAGCGCTTCGGAGTGTCTGGGAGCTCCAAGG 404  
QY 472 CTGTGATGAAGAAATCTTCAAAGTTTCTGCCGGTCAATTGGCTGGTCAATGTGTTTCTG 531

Db 405 TCCTCGCTAAGAGGAGCTGCTCTACGTGCCCTCATCGGCTGGACGTGTTCTCTGG 464  
QY 532 AGTATCTTTTCTGGAGAGAAGTTGGSCCAAGGATGAAGACACATTAAGTCAGGCATCC 591  
Db 465 AGATTGTCTCTCAAGCGGAAGTGGAGGAGGACCGGACACCGGTGGTGAAGGCTGA 524  
QY 592 AGCGACTGAGTGATTTCCCTCTTCCCTTTTGGCTAGCTCTCTTTGTAGAAGGAACGCGTT 651  
Db 525 GCGCGCTGTGGACTACCCCGAGTACATGTGTTTCTCTGTACTGGAGGGGACGCGCT 584  
QY 652 TTACACAGGCCAAACTATTAGCTGCTCAGGAATATGCCACTTCCACTGGATTGCTGTTT 711  
Db 585 TCACGGAGACCAAGCACCGCGTTAGCATGGAGGTGGCGGCTGTAAGGGGCTTCCCTGTCC 644  
QY 712 CTAGAAATGTTTGTATCCAAAGAACTAAGGGTTTGTCTGCGAGTAAGTCATATGCGCT 771  
Db 645 TCAAGTACACCTGTGCGCGGACCAAGGGCTTACCAACCGCAGTCAAGTGCCTCCGGG 704  
QY 772 CATTGTTCCTGCCATTTATGATGTAACAGTAGCCATCCCTAAGAGTTCCTCTGCTCCTA 831  
Db 705 GGACAGTCCGAGCTGTCTATGATGTAACCTGAACTTC---AGAGGAACAAGAACCCGT 761  
QY 832 CAATGCTAAGACTCTTCAAGGGACAACTTCAAGTGTGCTGATGTTTCAATCAAGAGCAT 891  
Db 762 CCTGTCTGGGATCCTCTACGGGAAGAGTACGAGCGGACATGTCGCTGAGGAGATTTC 821  
QY 892 TGATGAAGAACTGCCAGATACAGATGAGGCTGTTGCTCAATGGTGTGAGATATATTG 951  
Db 822 CTCTGGAACATCCCGCTGGATGAAGGAAGCAGCTCAGTGGCTTCATAAAGTGTACC 881  
QY 952 TGGCCCAAGGATGCTTTGTAGACAAACATATAGGCTGAGGGTACTTTTAGTGATCAGAGC 1011  
Db 882 AGGAGAAGACGCGCTCCAGGAGATATATATCAGAAGGGCATGTTCCAGGGGAGCAGT 941  
QY 1012 TGCAGGATGCTGTCGACC 1030  
Db 942 TTAAGCCTGCCCGGAGGCC 960

RESULT 10  
US-09-215-252-16  
; Sequence 16, Application US/09215252  
; Patent No. 6300487  
; GENERAL INFORMATION:  
; APPLICANT: LEUNG, David W.  
; APPLICANT: ADUREL, Daniel  
; APPLICANT: HOLLENBACK, David  
; TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE  
; FILE REFERENCE: 077319/0151  
; CURRENT APPLICATION NUMBER: US/09/215,252  
; CURRENT FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: US 08/618,651  
; PRIOR FILING DATE: 1996-03-19  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 1774  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (158)..(1291)  
US-09-215-252-16  
Query Match 6.7%; Score 100.2; DB 4; Length 1774;  
Best Local Similarity 47.0%; Pred. No. 3e-20;  
Matches 380; Conservative 0; Mismatches 423; Indels 6; Gaps 2;  
QY 159 TTGGCGCTGCTCTTCTTCGCTCCGCGCTCCTTGTGTAATCTCATTAGGCAATATGCTAT 218  
Db 206 TTCTGTACGTCTTTATTGCTCAGGCTAATCATCAACACCATTCAG---CTCTTCACT 262

QY 219 GTCGTGTAAGGCGGTGTCGAAAAGTTTGTACAGAGGATCAACCGGTTAGTAGCAGAG 278  
Db 263 CTCCTCTCTGCCCCATTAACAAGCAGCTCTTCCGGAAGATCAACTGCAGACTGTCTAT 322  
QY 279 CTCTTGTGGCTGGAGCTTGTATGGCTTATTGATTGTTGGGCGAGGATTAAGGTCCTAATA 338  
Db 323 TGCATCTCAAGCCAGCTGGTGTATGCTGCTGGAGTGGTTCGGGACGGAATGCACCATC 382  
QY 339 TTCACAGATCATGAACCTTTTCGTTTAAATGGGTAAGAGCATGCACATTGTGATAAGCAAT 398  
Db 383 TTCACGACCCCGCGCTACCTCAAGTATGGGAAGAAAATGCCATCGTGGTTCCTCAAC 442  
QY 399 CACAGAAGTGATATTGATTGGCTTGTGGATGGTTTTCAGCTCAGCGTTTCAGGTTTGTCTT 458  
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QY 459 GGCAGCACTCTAGCTGTGATGAAGAAATCTTCAAAAGTTTCTGCCGTCATTGGCTGGTCA 518  
Db 503 GGGGGCTCCAAGGTCCTGGCCAAAGAAAGAGCTGGCCTATGTCCCAATTATCGGCTGGATG 562  
QY 519 ATGTGGTTTCTGAGTATCTTTTCTGGAGAGAAGTTGGGCGCAAGGATGAAAGCAATTA 578  
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QY 579 AAGTCAGGATCCAGCACTGAGTGTATTCCTCTTCCCTTTTGGCTAGCTCTCTTTGTA 638  
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QY 639 GAAGGAACGCTTTTACACAGGCGCAACTATTAGTCTCAGGAATATGCCACTTCCACT 698  
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QY 699 GGATTGCTGTTCTAGAAATGTTTGTGATTTCAAGAACTAAGGGTTTGTCTGAGTA 758  
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QY 819 TCCCTGCTCCTACAATGCTAAGACTTCTCAAGGGACAACCTTCAAGTGGTGCATGTTTCA 878  
Db 863 ---GAAATCCAACACTGCTGGAGTCTCTAAACGGAAGAAATACCATGCAGATTGTAT 919  
QY 879 ATCAAGAGGCAATTTGATGAAGGAACCTGCCAGATACAGATGAGGCTGTTGCTCAATGGTGT 938  
Db 920 GTTAGGAGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGTCTCGGCTGGCTG 979  
QY 939 CGAGATATATTGTTGGCAAGGATGCTTT 967  
Db 980 CACAAGCTTACCAGGAGAAGGATGCTTT 1008

RESULT 11  
US-09-970-989A-16  
; Sequence 16, Application US/09970989A  
; Patent No. 6670143  
; GENERAL INFORMATION:  
; APPLICANT: LEUNG, David W.  
; APPLICANT: ADUREL, DANIEL  
; APPLICANT: HOLLENBACK, DAVID  
; TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE  
; FILE REFERENCE: 077319/0275  
; CURRENT APPLICATION NUMBER: US/09/970,989A  
; CURRENT FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: 09/215,252  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 08/618,651  
; PRIOR FILING DATE: 1996-03-19  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 1774

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (158) .. (1291)
US-09-970-989A-16

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Query Match	6.7%	Score 100.2;	DB 4;	Length 1774;
Best Local Similarity	47.0%	Pred. No. 3e-20;		
Matches 380; Conservative	0;	Mismatches 423;	Indels 6;	Gaps 2;

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Qy	219	GTCGTCGTAAAGCCCGGTGTCGAAAAGTTTGTACAGAAGATCAACCGGTACTAGCAGAG	278
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Qy	279	CTCTTGTGGCTGGAGCTTGATGGCTTATTGATTGGTGGCGCAGGAGTTAAGTCCAAATA	338
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QY			TTT	CACAGATCATGAAACCTTTTCGT	TAA	TGGTAAAGAGCATGCAC	TTTGTA	TAAAGCAAT	398
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QY	579	AAGTCAGGCATCCACGCGACTGAGTGATTCCCTCTCTTCCCCTTTGGCTAGCTCTCTTTGTA	638
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Qy	639	GAAGGAACGCGTTTTCACACAGGCCAAACTATTAGCTGCTCAGGAATATGCCACTTCCACT	698
Db	683	GAGGGCACACCGTTTCACGGAAGAAGCATGAGATCAGCATGCAGGTGGCCCGGCCAAG	742

QY	699	GGATTGCCTGTTCCCTAGAAATGTTTGTATTC	AAAGAACTAAGGGTTTTGTTTCTGCAGTA	758
Db	743	GGGCTGCCTCGCCTCAAGCATCAGCTGTTGCCACGAA	CCAAAGGGTTTCGCCATCACCGTG	802

QY	759	AGTCATATGCGCTCATTTGTTCTTGCCCATTTATGATGTAACAGTAGCCATCCCTAAGAGT	818
Dδ	803	AGGAGCTTGAGAAATGTAGTTTCAGCTGTATATGCTGTACACTCAATTTTCAGAAATAAT	862

QY	819	TCCCTGCTCCTACAATGCTAAGACTCTTCAAGGACAACCTTCAGTGGTGCATGCTCAT	878
Dδ	863	---GAAAAATCCAACTGCTGGAGTCCTAAACGGAAGAAATACCATGCAGATTGTGAT	919

[illegible]

QY	939	CGAGATATATTTGTGGCCAAGGATGCTTT	967
db	980	CACAAGCTCTACCAAGGAGAAGGATGCCTT	1008

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; Sequence 1820, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:

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Db	1468	CATTTTCCTGTTTCAGCATGTTATATTCTTATAAATAAAAGCAAAAGTCAAAATATGAAA	1527
Qy	1479	AAAAAAAAAAAAAAAAAAAA	1496
Db	1528	AAAAAAAAAAAAAAAAAAAA	1545

Search completed: July 9, 2004, 21:49:47  
Job time : 99 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 9, 2004, 21:00:33 ; Search time 519 Seconds  
(without alignments)  
14067.586 Million cell updates/sec

Title: US-09-914-098-55  
Perfect score: 1498  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3183909 seqs, 2436941669 residues

Total number of hits satisfying chosen parameters: 6367818

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1347.2	89.9	1593	13	US-10-424-599-135471 Sequence 135471, A
2	1131	75.5	1131	13	US-10-425-114-10439 Sequence 10439, A
3	1108.4	74.0	1394	13	US-10-424-599-135449 Sequence 135449, A
4	1107	73.9	1302	13	US-10-425-114-6209 Sequence 6209, Ap
5	1017	67.9	1750	13	US-10-424-599-67243 Sequence 67243, A
6	866.8	57.9	1583	13	US-10-425-114-11471 Sequence 11471, A
7	849.4	56.7	1436	13	US-10-425-114-9374 Sequence 9374, Ap
8	642.2	42.9	1515	8	US-08-818-581B-3 Sequence 3, Appli
9	552.6	36.9	1709	13	US-10-425-114-28840 Sequence 28840, A
10	550.8	36.8	1829	17	US-10-437-963-27991 Sequence 27991, A
11	549.4	36.7	1550	13	US-10-425-114-26574 Sequence 26574, A
12	453.6	30.3	1220	13	US-10-425-114-2048 Sequence 2048, Ap
13	437.6	29.2	1646	13	US-10-425-114-16071 Sequence 16071, A
14	413.6	27.6	717	13	US-10-424-599-135460 Sequence 135460, A

15	388.8	26.0	581	17	US-10-021-323-14948 Sequence 14948, A
16	372.6	24.9	603	17	US-10-021-323-617 Sequence 617, App
17	368.2	24.6	1149	13	US-10-425-114-35660 Sequence 35660, A
18	366.4	24.5	571	13	US-10-424-599-51032 Sequence 51032, A
19	285.8	19.1	459	13	US-10-424-599-123654 Sequence 123654, A
20	233.8	15.6	501	13	US-10-424-599-87069 Sequence 87069, A
21	150	10.0	279	9	US-09-294-093B-2887 Sequence 2887, Ap
22	125	8.3	467	13	US-10-424-599-70805 Sequence 70805, A
23	121.8	8.1	1660	9	US-09-970-989-12 Sequence 12, Appl
24	121.8	8.1	1660	13	US-10-667-494-12 Sequence 12, Appl
25	121.8	8.1	1660	17	US-10-667-462-12 Sequence 12, Appl
26	121.8	8.1	1660	17	US-10-667-464-12 Sequence 12, Appl
27	120.2	8.0	1128	9	US-09-798-029-13 Sequence 13, Appl
28	120.2	8.0	1769	15	US-10-037-270-841 Sequence 841, App
29	120.2	8.0	1769	16	US-10-117-722-841 Sequence 841, App
30	120.2	8.0	1832	9	US-09-798-029-5 Sequence 5, Appli
31	120.2	8.0	1960	13	US-10-296-606-22 Sequence 22, Appl
32	120.2	8.0	3060	10	US-09-946-174-296 Sequence 296, App
33	120.2	8.0	3060	12	US-10-015-395A-296 Sequence 296, App
34	120.2	8.0	3060	13	US-10-206-915-337 Sequence 337, App
35	120.2	8.0	3060	13	US-10-199-670-337 Sequence 337, App
36	120.2	8.0	3060	13	US-10-201-858-337 Sequence 337, App
37	120.2	8.0	3060	13	US-10-205-890-337 Sequence 337, App
38	120.2	8.0	3060	13	US-10-208-024-337 Sequence 337, App
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41	120.2	8.0	3060	13	US-10-176-483-337 Sequence 337, App
42	120.2	8.0	3060	13	US-10-176-749-337 Sequence 337, App
43	120.2	8.0	3060	13	US-10-176-914-337 Sequence 337, App
44	120.2	8.0	3060	13	US-10-176-915-337 Sequence 337, App
45	120.2	8.0	3060	13	US-10-006-485A-296 Sequence 296, App

ALIGNMENTS

RESULT 1  
US-10-424-599-135471  
; Sequence 135471, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 135471  
; LENGTH: 1593  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_9333C.1  
US-10-424-599-135471

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Qy	177	GCCTCCGGCCCTCCTTGTAACTCATTCAGGCAATATGCTATGTCGTAGGCCCGGTG	236	
Db	285	GCCTCCGGCCCTCCTTGTAACTCATTCAGGCAATATGCTATGTCGTAGGCCCGGTG	344	
Qy	237	TCGAAAGTTTGTACAGAAGGATCAACCGGGTAGTACAGAGCTCTTGTGGCTGGAGCTT	296	

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Db 465 TTTCGTTTAAATGGTAAAGAGATGCACCTTGTGATAGCAATCAACAGAGTGTATTCAT 524

QY 417 TGGCTTGTGGATGGGTTTTCAGCTCAGCGTTTTCAGGTTTGTCTGGCAGCACTCTAGCTGTG 476

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Db 585 ATGAAGAAATCTTCAAAGTTTCTGCCGTTTTCAGCTTGGCTGGTCAATGTGGTTTCTGAGTAT 644

QY 537 CTTTCTTGAGAGAAAGTTGGGCCCAAGGATGAAAGCACATTAAGTCAAGGATCCAGCGA 596

Db 645 CTTTCTTGAGAGAAAGTTGGGCCCAAGGATGAAAGCACATTAAGTCAAGGATCCAGCGA 704

QY 597 CTGAGTGAATTCCTCTTCCCTTTTGGCTAGCTCTCTTGTAGAGGAAACGGTTTACA 656

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QY 897 AAGGAACCTGCCAGATACAGATGAGGCTGTTGCTCAATGGTGTGAGATATATTTGTGGCC 956

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QY 957 AAGGATGCTTTGTTAGACAAACATATGGCTGAGGTTACTTTTAGTGATCAAGAGTGCAG 1016

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RESULT 2

US-10-425-114-10439

; Sequence 10439, Application US/10425114

; Publication No. US2004003488A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingsong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 10439

; LENGTH: 1131

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: 700909008\_FLI

US-10-425-114-10439

Query Match 75.5%; Score 1131; DB 13; Length 1131;

Best Local Similarity 100.0%; Pred. No. 4.8e-287;

Matches 1131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 289 TGGAGCTTGTATGGCTTATGATTGGTGGGCGAGGATTAAGTCCAAATATTCACAGATC 348

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QY 349 ATGAAACCTTTTCGTTTAAATGGTAAAGAGCATGCATTTGTGATAGCAATCAAGAGTG 408

Db 121 ATGAAACCTTTTCGTTTAAATGGTAAAGAGCATGCATTTGTGATAGCAATCAAGAGTG 180

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Db 721 TTGTGGCCAAAGGATGCTTTGTTAGACAAACATATGGCTGAGGGTACTTTTAGTGATCAAG 780  
Qy 1009 AGCTGCAGGATACTGGTCGACCAATAAAGTCTCTTCTGGTAGTTATATCTTTGGGCGTGC 1068  
Db 781 AGCTGCAGGATACTGGTCGACCAATAAAGTCTCTTCTGGTAGTTATATCTTTGGGCGTGC 840  
Qy 1069 TGGTTGTTGGGGTCTGTAAAGTTCCTGCAATGGTCTTCGTTACTCTCTTCTCGGAAGG 1128  
Db 841 TGGTTGTTGGGGTCTGTAAAGTTCCTGCAATGGTCTTCGTTACTCTCTTCTCGGAAGG 900  
Qy 1129 GTGTTGCATTTTCAGCTTTTGGTTTGGCAGTTGTTACTGCACTTATGCAAAATTCGTATTC 1188  
Db 901 GTGTTGCATTTTCAGCTTTTGGTTTGGCAGTTGTTACTGCACTTATGCAAAATTCGTATTC 960  
Qy 1189 AATTCTCAGCTCAGAGCGTTCAAAACCGGCCAAGATCGTGCCTGCAAGTCAAAAAACA 1248  
Db 961 AATTCTCAGCTCAGAGCGTTCAAAACCGGCCAAGATCGTGCCTGCAAGTCAAAAAACA 1020  
Qy 1249 AGGGGTCTTGATTTATTTGGCGAACTTAAAGTTGCAATTTATGTGTGATGAGTGACTCATG 1308  
Db 1021 AGGGGTCTTGATTTATTTGGCGAACTTAAAGTTGCAATTTATGTGTGATGAGTGACTCATG 1080  
Qy 1309 TAATACTCATTTATTTGCTTTCAACATCTTATCATAGTATGCTTCTATTCT 1359  
Db 1081 TAATACTCATTTATTTGCTTTCAACATCTTATCATAGTATGCTTCTATTCT 1131

RESULT 3  
US-10-424-599-135449  
; Sequence 135449, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 135449  
; LENGTH: 1394  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_9331C.1  
US-10-424-599-135449

Query Match 74.0%; Score 1108.4; DB 13; Length 1394;  
Best Local Similarity 88.0%; Pred. No. 4.9e-281;  
Matches 1295; Conservative 0; Mismatches 1; Indels 176; Gaps 1;  
Qy 5 GAGGTTCCGTTGCTGACCTCGGAATCCAAAGAGGAACTCAGGTGTTTCGT 64  
Db 90 GTGGTTCCGTTGCTGACCTCGGAATCCAAAGAGGAACTCAGGTGTTTCGT 149

Qy 65 TCGGTTGTGCTCTGCTCTGCTCCTTTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 124  
Db 150 TCGGTTGTGCTCTGCTCTGCTCCTTTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 209  
Qy 125 CATGGCTATTGCAGCAGCGGCGGTGGTGATCCATTGGGCTGCTCTTCTTCGCCTCCGG 184  
Db 210 CATGGCTATTGCAGCAGCGGCGGTGGTGATCCATTGGGCTGCTCTTCTTCGCCTCCGG 269  
Qy 185 CCTCCTTGTAAATCTCATTACAGGCAATATGCTATGTCTGCTAAGCCGCGGTGTCGAAAAG 244  
Db 270 CCTCCTTGTAAATCTCATTACAGGCAATATGCTATGTCTGCTAAGCCGCGGTGTCGAAAAG 329  
Qy 245 TTTGTACAGAAAGGATCAACCGGGTAGTAGCAGAGCTCTTGTGGCTGGAGCTTGTATGGCT 304  
Db 330 TTTGTACAGAAAGGATCAACCGGGTAGTAGCAGAGCTCTTGTGGCTGGAGCTTGTATGGCT 389  
Qy 305 TATTGATTGGTGGGCAGGAGTTAAGTCCAAATATTACAGATCATGAAACCTTTTCGTTT 364  
Db 390 TATTGATTGGTGGGCAGGAGTTAAGTCCAAATATTACAGATCATGAAACCTTTTCGTTT 449  
Qy 365 AATGGGTAAAGAGCATGCACCTGTGATAAGCAATACAGAAAGTATATTGATTGGCTTGT 424  
Db 450 AATGGGTAAAGAGCATGCACCTGTGATAAGCAATACAGAAAGTATATTGATTGGCTTGT 509  
Qy 425 TGGATGGGTTTCAGCTCAGCGTTTCAGGTTGCTTGGCAGCACTCTAGCTGTGATGAAGAA 484  
Db 510 TGGATGGGTTTCAGCTCAGCGTTTCAGGTTGCTTGGCAGCACTCTAGCTGTGATGAAGAA 569  
Qy 485 ATCTTCAAAGTTTCTGCCGTCAATTGGCTGGTCAATGTGGTTTCTGAGTATCTTTTCT 544  
Db 570 ATCTTCAAAGTTTCTGCCGTCAATTGGCTGGTCAATGTGGTTTCTGAGTATCTTTTCT 629  
Qy 545 GGAGAGAAGTTGGGCCAAGGATGAAAGCACATTAAGTCAGGCATCCAGCGACTGAGTGA 604  
Db 630 GGAGAGAAGTTGGGCCAAGGATGAAAGCACATTAAGTCAGGCATCCAGCGACTGAGTGA 689  
Qy 605 TTTCCCTCTTCCCTTTTGGCTAGCTCTCTTTGTAGAAGGACGCGTTTACACAGGCCAA 664  
Db 690 TTTCCCTCTTCCCTTTTGGCTAGCTCTCTTTGTAGAAGGACGCGTTTACACAGGCCAA 749  
Qy 665 ACTATTAGCTGCTCAGGAATATGCCACTTCCACTGGATTGCTGCTTCCCTAGAAATGTTT 724  
Db 750 ACTATTAGCTGCTCAGGAATATGCCACTTCCACTGGATTGCTGCTTCCCTAGAAATGTTT 809  
Qy 725 GATTTCAAGAACTAAGGTTTGTGTTTCTGCAGTAAGTCATATGCGCTCATTTGTTCTCTGC 784  
Db 810 GATTTCAAGAACTAAGGTTTGTGTTTCTGCAGTAAGTCATATGCGCTCATTTGTTCTCTGC 869  
Qy 785 CATTATGATGTAACAGTAGCCATCCCTAAGAGTTCCTGCTCCTACAAATGCTAAGACT 844  
Db 870 CATTATGATGTAACAGTAGCCATCCCTAAGAGTTCCTGCTCCTACAAATGCTAAGACT 929  
Qy 845 CTTCAAGGGACAACTTCAAGTGGTGCATGTTTCATATCAAGAGGCAATTTGATGAAGGAACT 904  
Db 930 CTTCAAGGGACAACTTCAAGTGGTGCATGTTTTCATATCAAGAGGCAATTTGATGAAGGAACT 961  
Qy 905 GCCAGATACAGATGAGGCTGTTGCTCAATGGTGTGAGATATATTGTTGGCCAAAGGATGC 964  
Db 962 ----- 961  
Qy 965 TTTGTTAGACAAACATATGGCTGAGGGTACTTTTAGTGATCAAGAGCTGCAGGATCTGG 1024  
Db 962 ----- 961  
Qy 1025 TCGACCAATAAAGTCTCTTCTGGTGTGTTATATCTGGGCGTGTCTGGTGTGTTGGGGGTC 1084  
Db 962 -----ATACTTGGGCGTGTCTGGTGTGTTGGGGGTC 993  
Qy 1085 TGTAAAGTTTCTGCAATGGTCTTCGTTACTCTCTTCTGGAAGGTTGTTGCAATTTTCAGC 1144  
Db 994 TGTAAAGTTTCTGCAATGGTCTTCGTTACTCTCTTCTGGAAGGTTGTTGCAATTTTCAGC 1053

QY 1145 TTTTGGTTTGGCAGTTGTTACTGCACTTATGCAATTTCTGATTCAATTTCTCACAGTCAGA 1204  
DB 1054 TTTTGGTTTGGCAGTTGTTACTGCACTTATGCAATTTCTGATTCAATTTCTCACAGTCAGA 1113  
QY 1205 GCGTTCAAAACCCGGCCAAAGATCGTGCCTGCAAAAGTCAAAAAACAAGGGTCTTTGATTAT 1264  
DB 1114 GCGTTCAAAACCCGGCCAAAGATCGTGCCTGCAAAAGTCAAAAAACAAGGGTCTTTGATTAT 1173  
QY 1265 TTGGCGAACTTAAAGTTGCAATTTATGTGATGAGTGACTCATGTAAATACTCAATATTTT 1324  
DB 1174 TTGGCGAACTTAAAGTTGCAATTTATGTGATGAGTGACTCATGTAAATACTCAATATTTT 1233  
QY 1325 GCTTTCAACATCTTATCATAGTATGCTTCTATTTCTATATATGTACTATTAATGCTTA 1384  
DB 1234 GCTTTCAACATCTTATCATAGTATGCTTCTATTTCTATATATGTACTATTAATGCTTA 1293  
QY 1385 TCGATTCAATGTTTTTAAATTAATTAAGGATATCCTTTTGTATTTGACAGTCTAGGGGATGG 1444  
DB 1294 TCGATTCAATGTTTTTAAATTAATTAAGGATATCCTTTTGTATTTGACAGTCTAGGGGATGG 1353  
QY 1445 CCTAGAAAAATTCAACCACTATTTTATTTTA 1476  
DB 1354 CCTAGAAAAATTCAACCACTATTTTATTTTA 1385

RESULT 4

US-10-425-114-6209  
; Sequence 6209, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 6209  
; LENGTH: 1302  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700557018\_FLI  
US-10-425-114-6209

Query Match 73.9%; Score 1107; DB 13; Length 1302;  
Best Local Similarity 88.0%; Pred. No. 1.le-280;  
Matches 1293; Conservative 0; Mismatches 0; Indels 176; Gaps 1;

QY 8 GTTCCGTTTGTGCTGACCTCGGAAATCCAAAGAGGGAACCTCACGGTGTTCGTTGC 67  
DB 1 GTTCCGTTTGTGCTGACCTCGGAAATCCAAAGAGGGAACCTCACGGTGTTCGTTGC 60  
QY 68 GTTGTGCTGCTGCTGCTCCTTTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 127  
DB 61 GTTGTGCTGCTGCTGCTCCTTTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 120  
QY 128 GGCTATTCAGCAGCGCGCGTGGTACCATTTGGGCTGCTCTTCTTCCCTCCGCGCT 187  
DB 121 GGCTATTCAGCAGCGCGCGTGGTACCATTTGGGCTGCTCTTCTTCCCTCCGCGCT 180  
QY 188 CTTGTTAATCTCATTACAGGCAATATGCTATGTCGTAAAGCGGCTGTCGAAAGTTT 247  
DB 181 CTTGTTAATCTCATTACAGGCAATATGCTATGTCGTAAAGCGGCTGTCGAAAGTTT 240  
QY 248 GTACAGAAGGATCAACCGGGTAGTACAGAGCTCTTGTGGCTGGAGCTTGTATGGCTTAT 307  
DB 241 GTACAGAAGGATCAACCGGGTAGTACAGAGCTCTTGTGGCTGGAGCTTGTATGGCTTAT 300

QY 308 TGATTGGTGGCAGGATTAAAGTCCAAATATTTCACAGATCATGAAACCTTTTCGTTTAAAT 367  
DB 301 TGATTGGTGGCAGGATTAAAGTCCAAATATTTCACAGATCATGAAACCTTTTCGTTTAAAT 360  
QY 368 GGGTAAAGAGCATGCACCTTGTGATAAGCAATCACAGAAAGTGATATTGATTGGCTTGG 427  
DB 361 GGGTAAAGAGCATGCACCTTGTGATAAGCAATCACAGAAAGTGATATTGATTGGCTTGG 420  
QY 428 ATGGGTTTCAGCTCAGCGTTCAGGTTGCTTGGCAGCACTCTAGCTGTGATGAAGAAATC 487  
DB 421 ATGGGTTTCAGCTCAGCGTTCAGGTTGCTTGGCAGCACTCTAGCTGTGATGAAGAAATC 480  
QY 488 TTCAAAGTTTCTGCCGTCATTGGCTGCTCAATGTGTTTCTGAGTATCTTTTCTGGA 547  
DB 481 TTCAAAGTTTCTGCCGTCATTGGCTGCTCAATGTGTTTCTGAGTATCTTTTCTGGA 540  
QY 548 GAGAAGTTGGGCCAAGGATGAAAGCAGATTAAAGTCAGGCATCCAGGCACTGAGTGATTT 607  
DB 541 GAGAAGTTGGGCCAAGGATGAAAGCAGATTAAAGTCAGGCATCCAGGCACTGAGTGATTT 600  
QY 608 CCTCTTCCCTTTTGGCTAGCTCTCTTTGTAGAAAGAACGCTTTTACACAGGCCAACT 667  
DB 601 CCTCTTCCCTTTTGGCTAGCTCTCTTTGTAGAAAGAACGCTTTTACACAGGCCAACT 660  
QY 668 ATTAGCTGCTCAGGAATATGCCACTTCCACTGGATTGCTGTTCTTAGAAATGTTTGTAT 727  
DB 661 ATTAGCTGCTCAGGAATATGCCACTTCCACTGGATTGCTGTTCTTAGAAATGTTTGTAT 720  
QY 728 TCCAAGAACTAAGGGTTTGTCTTCTGAGTAAGTCATATGCGCTCATTTGTTCTCGCAT 787  
DB 721 TCCAAGAACTAAGGGTTTGTCTTCTGAGTAAGTCATATGCGCTCATTTGTTCTCGCAT 780  
QY 788 TTATGATGTAACAGTAGCCATCCCTAAGAGTTCCCTGCTCCTACAATGCTAAGACTCTT 847  
DB 781 TTATGATGTAACAGTAGCCATCCCTAAGAGTTCCCTGCTCCTACAATGCTAAGACTCTT 840  
QY 848 CAAGGACAACTTCAAGTGTGATGTTTCATATCAAGAGGCAATTTGATGAAGGAAGTCC 907  
DB 841 CAAGGACAACTTCAAGTGTGATGTTTCATATCAAGAGGCAATTTGATGAAGGAAGTCC 869  
QY 908 AGATACAGATGAGGCTGTTGCTCAATGGTGTGAGATATATTGTCGCCAAGGATGCTTT 967  
DB 870 ----- 869  
QY 968 GTTAGACAAACATATGGCTGAGGGTACTTTTAGTATCAAGAGTGCAGGATACTGTCG 1027  
DB 870 ----- 869  
QY 1028 ACCAATAAGTCTCTTCTGGTAGTTATATATCTTGGGCGTGTCTGTTGTTGCGGGTCTGT 1087  
DB 870 -----ATATCTTGGGCGTGTCTGTTGTTGCGGGTCTGT 904  
QY 1088 AAAGTTCTGCAATGGTCTTCTGTTACTCTCTTCTGGAAGGGTGTGCAATTTTCAGCTTT 1147  
DB 905 AAAGTTCTGCAATGGTCTTCTGTTACTCTCTTCTGGAAGGGTGTGCAATTTTCAGCTTT 964  
QY 1148 TGGTTTGGCAGTTGTTACTGCACTTATGCAAAATTTCTGATTCAATTTCTACAGTACAGCG 1207  
DB 965 TGGTTTGGCAGTTGTTACTGCACTTATGCAAAATTTCTGATTCAATTTCTACAGTACAGCG 1024  
QY 1208 TTCAAAACCCGGCCCAAGATCGTGCCTGCAAAAGTCAAAAAACAAGGGTCTTGAATTATTG 1267  
DB 1025 TTCAAAACCCGGCCCAAGATCGTGCCTGCAAAAGTCAAAAAACAAGGGTCTTGAATTATTG 1084  
QY 1268 GCGAACTTAAAGTTGCAATTTATGTGTGATGAGTGAATCAATTAATCAATTAATTTGCT 1327  
DB 1085 GCGAACTTAAAGTTGCAATTTATGTGTGATGAGTGAATCAATTAATCAATTAATTTGCT 1144  
QY 1328 TTCAACATCTTATCATAGTATGCTTCTATTTCTATATATGTAATGATGCTTATCG 1387  
DB 1145 TTCAACATCTTATCATAGTATGCTTCTATTTCTATATATGTAATGATGCTTATCG 1204



QY 1388 ATTCATTGTTTAAATTAAGGATATCCTTTTGTATTGACAGTCTAGGGATGCGCT 1447  
Db 1205 ATTCATTGTTTAAATTAAGGATATCCTTTTGTATTGACAGTCTAGGGATGCGCT 1264  
QY 1448 AGAAAAATCAACCACCTATTTTATTTA 1476  
Db 1265 AGAAAAATCAACCACCTATTTTATTTA 1293

RESULT 5  
US-10-424-599-67243  
; Sequence 67243, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 67243  
; LENGTH: 1750  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_31735C.1  
US-10-424-599-67243

Query Match 67.9%; Score 1017; DB 13; Length 1750;  
Best Local Similarity 90.5%; Pred. No. 6.7e-257;  
Matches 1119; Conservative 0; Mismatches 115; Indels 3; Gaps 3;

QY 1 GCACGAGGTTCCGTTTGTGACCTGACCTCGGAAATCCAAAGAGGGAACCTCACGGTGT 60  
Db 104 GAATGCGGTGCGTTTACTGACCTGACCTCGGAAAT-CAAAGAGCGAAACTCCCGGTG-T 161  
QY 61 TCGTTGCGTTGTGCTCTGCTCTGCTCTGCTTGGGCGCTGGGCTGGGCTGGGCTGGGC 120  
Db 162 TCGTTGCGTTGTGCTCTGCTCTGCTCTGCTTGGGCGCTGGGCTGGGCTGGGCTGGGC 221  
QY 121 TGGGCATGGCTATTGCAGACGGCGCGGTGGTGGTACCAATGGGCGCTGCTTCTTCGCGCT 180  
Db 222 TGGGCATGGCTATTGACTGCAG-TGCTGTGGTGGTCCCAATGGGCGCTGCTTCTTCGCTT 280  
QY 181 CCGGCCCTCCTGTTAATCTCATTAGGCAATATGCTATGCTCGTAAAGCCGGTGTGCA 240  
Db 281 CCGGCCCTCATCGTTTAACTCATTAGGCAATATGCTATGCTGTTGTACGCCCGGTGTGCA 340  
QY 241 AAAGTTTGTACAGAAAGGATCAACCGGGTAGTAGCAGAGCTCTTGTGGCTGGAGCTTGAT 300  
Db 341 AGAATTTGTACCGCGGATGAACAGGGTGGTGGTGAACCTCCTGTGGCTGGAGCTCGTTT 400  
QY 301 GGCTTATTGATTGGTGGCAGGAGTTAAGGTCCAAATATTCACAGATCATGAAACCTTTC 360  
Db 401 GGATTATTGATTGGTGGCTGGTGTAAAGTCCAAAGTATTCACAGATCCTGAAACCTTTC 460  
QY 361 GTTTAATGGGTAAAGAGCATGCACCTTGTGATAAGCAATCACAGAAGTATGATTGGC 420  
Db 461 ATTCAATGGGTAAAGAGCATGCTCTTGTCTATATCCAATCACAGAAGTACATTGATTGGC 520  
QY 421 TTGTTGGATGGGTTTCAGCTCAGCGTTTCAGGTTGCTTTGGCAGCACTCTAGCTGTGATGA 480  
Db 521 TTGTTGGATGGGTTTATGCTCAGCGTTTCAGGTTGCTTTGGCAGCACTCTTGTGTGATGA 580  
QY 481 AGAAATCTTCAAAGTTTCTGCCGGTCAATGGCTGGTCAATGTGGTTTCTAGTATCTTT 540  
Db 581 AGAAATCTTCAAAGTTTCTACCGGTCAATGGTGGTGGTCAATGTGGTTTCTGAATATCTTT 640  
QY 541 TTCTGGAGAGAGTTGGGCCCAAGGATGAAGACACATTAAGTCAAGGCATCCAGCGACTGA 600

Db 641 TCCTGGAGAGAAAGTTGGCCAAAGATGAACGCACATTAAGTCAGGCCCTACAGCAACTGA 700  
QY 601 GTGATTTCCCTCTTCCCTTTTGGCTAGCTCTCTTTGTAGAGGAACGCGTTTACACAGG 660  
Db 701 GGGATTTCCCTCTTCCCTTTTGGCTCTCTTTGTAGAGGAACCTCGCTTTACACAGG 760  
QY 661 CCAAACTATTAGCTGCTCAGGAATATGCCACTTCCACTGGATTGCCTGCTCCTAGAAATG 720  
Db 761 CCAAACTATTAGCTGCTCAGAGATATGACGCTCAGCTGGATTGCCCTGTTCCAAAGAAATG 820  
QY 721 TTTTGATTTCAAAGAACTAAGGGTTTGTGTTTCTGAGTAAGTACATATGCGCTCATTTGTTT 780  
Db 821 TTTTGATTTCAAAGAACTAAGGGTTTGTGTTTCTGAGTAAGTACATATGCGCTCGTTTGTTC 880  
QY 781 CTGCCATTTATGATGTAAACAGTAGCCATCCCTAAGAGTTCCCTGCTCCTACAAATGCTAA 840  
Db 881 CTGCCATTTATGATGTAACTGTGGCAATTTCCCAAGAGTTCACCTGCTCCTACAAATGCTAA 940  
QY 841 GACTCTTCAAGGGACAACCTTCAGTGGTGCATGTTTCATATCAAGAGGCAATTTGATGAAGG 900  
Db 941 GACTCTTCAAGGGACAACCTTCAGTGGTGCATGTTTCATATCAAGAGGCAATTTGATGAAGG 1000  
QY 901 AACTGCCAGATACAGATGAGGCTGTTGCTCAATGGTGTGAGATATATTTTGGCCCAAGG 960  
Db 1001 AACTGCCAGATACAGATGAGGCTGTTGCTCAATGGTGTGAGATATATTTTGGCCCAAGG 1060  
QY 961 ATGCTTTGTTAGACAAACATATGGCTGAGGCTACTTTTAGTGATCAAGAGCTGCAGGATA 1020  
Db 1061 ATGCTTTGTTAGACAAACATATGGCTGAGGACACATTTTAGTGATCAAGAGCTGCAGGATA 1120  
QY 1021 CTGGTCGACCAATAAAGTCTCTTCTGTTAGTTATATCTTGGGCGTGTCTGTTGTTGCGG 1080  
Db 1121 CTGGTCGACCAATAAAGTCTCTTCTGTTAGTTATATCTTGGGCGTGTCTGTTGTTGCGG 1180  
QY 1081 GGTCTGTAAAGTTCCTGCAATGGTCTTCTGTTACTCTCTTCTGGAAGGGTGTGCAATTTT 1140  
Db 1181 GGGTCGTAAAGTTCCTCAATGGTCTTCTCACTACTATCTCTCTGGAAGGGTGTGCAATTTT 1240  
QY 1141 CAGCTTTTGGTTGGCAGTTGTTACTGCACTTATGCAATTCATGCAATTTCTGATTCACAGT 1200  
Db 1241 CAGCATTTGTTGGAGTTGTCACTCTACTCATGCACATCTTGATCATGTTCTCACAAT 1300  
QY 1201 CAGAGCGTTCAAACCCCGCCCAAGATCGTGCCCTGCAAA 1237  
Db 1301 CTGAGCGTTCAACCCCTTCCAAGGTTGCCCTACAAA 1337

RESULT 6  
US-10-425-114-11471  
; Sequence 11471, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 11471  
; LENGTH: 1583  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 701127504\_FLI  
US-10-425-114-11471



```

; INFORMATION FOR SEQ ID NO: 3:
;
; SEQUENCE CHARACTERISTICS:
;
;   LENGTH: 1515 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;
;   MOLECULE TYPE: cDNA
;
;   FEATURE:
;
;     NAME/KEY: CDS
;     LOCATION: 182..1316
;
US-08-0818-581B-3

```

Query Match	42.9%	Score 642.2;	DB 8;	Length 1515;
Best Local Similarity	73.4%	Pred. No. 3.2e-158;		
Matches 821; Conservative	0;	Mismatches 298;	Indels 0;	Gaps 0;

Qy	106	TGGCTGGGCTGGCTGGGCGATGGCTATTGCAGCAGCGGCCGTGGTGGTACCATTTGGGCC	165
Db	162	TAGCCCGAGCTAAAGCTGCCATGGCGATCCCTGCTGCAGCTTTCATCGTACCAATAAGTC	221
	166	TGCTCTTCTTCGCGCTCGGCGCTCCTTGTTAATCTCAATTCAGGCAATATGCTATGTCGTG	225
Db	222	TTCTTTTTTTCATGTCAGGCGCTCGTTGTCAATTTCAATTCAGGCAGTCTTCTATGTTCTTG	281
	226	TAAGGCCGGTGTGCAAAAAGTTTTGTACACAAGGATCAACCGGGTAGTAGCAGAGCTCTTGT	285
Db	282	TTCGGCGCTATTTCTAAGGACACATACAGAAGGATCAATACGTTGGTGGCAGAAATGTTGT	341
	286	GGCTGGAGCTTGATGGCTTATTGATTGGTGGCAGGAGTTAAGGTCCTAAATATTCACAG	345
Db	342	GGCTAGAACTTGATGGGTCATTGATTGGTGGCAGGCGTTAAGGTCCTAATATATACTG	401
	346	ATCATGAAACCTTTCGTTTAATGGGTAAGAGCATGCACCTTGATATAAGCAATCACAGAA	405
Db	402	ATACTGAGCTTTCCGCTAATGGGTAAGAAACATGCACCTCTTAATATGCAACCCACAGAA	461
	406	GTGATATTGATTGGCTTGTGGATGGGTTTCAGCTCAGCGTTCAGGTTGTCTTGGCAGCA	465
Db	462	GTGACATTGACTGGCTCATTGGATGGGTCCTAGCACAGCGATCGGCTGCCTCAGTTCCT	521
	466	CTCTAGCTGTGATGAAGAAATCTTCAAAGTTTCTGCCGTCATTGGCTGGTCAATGTGGT	525
Db	522	CAATAGCTGTTATGAAGAAGTCATCCAAATTTCTCCCGTAATAGGTTGGTCTATGTGGT	581
	526	TTTCTGAGTATCTTTTTCTGGAGAGAAGTTGGCCAAAGGATGAAAGCAATTAAGTCAG	585
Db	582	TTTCCGAATATCTCTTTCTCGAGAGGAACCTGGCCAAAGATGAAAACATTTAAAGTCAG	641
	586	GCATCCAGCGACTGAGTGATTTCCCTCTTCCCTTTTGGCTAGCTCTCTTTGTAGAAGGAA	645
Db	642	GTCTCCAGCGGCTGAATGACTTCCCTAAGCCTTTTGGTTAGCTCTGTTGTGGAAGGAA	701
	646	CGCGTTTACACAGGCCAAACTATTAGCTGCTCAGGAATATGCCACTTCCACTGGATTGC	705
Db	702	CTCGTTTCAGAAAGCAAACTTCTAGCTGCTCAGGAATATGCAGCCTCTGCAGGATTAC	761
	706	CTGTTCTAGAAAATGTTTGATTCCAGAACTAAGGGTTTTGTTTCTGCAGTAAGTCATA	765
Db	762	CCGTGCTCGAAATGTTCTGATTCTCTCGTACGAAGGGCTTTGTGTGAGCCGTTAGTAACA	821
	766	TGCGCTCAATTTGTTCCCTGCCATTTATGATGTAAACAGTAGCCATCCCTAAGAGTTCCCTG	825
Db	822	TGCGCTCAATTTGTCCAGCTATCTATGACTTGACAGTGCCTATCCCTAAAACCCACGGAAC	881
	826	CTCCTACAAATGCTAAGACTCTTCAAGGACAAACCTTCAGTGGTGCAATGTTCAATCAAGA	885
Db	882	AACCTACAAATGCTCAGACTGTTTCAGGGGAAATCTTCTGTGGTACACGCTACACCTTAAGC	941
	886	GGCAATTTGATGAAGGAACCTGCCAGATACAGATGAGGCTGTTGCTCAATGGTGTGAGATA	945
Db	942	GGCAATTTGATGAAGGACTTGCCTAAACACAGATGACGGTGTGTCACAGTGGTGTAAAGATC	1001
	946	TATTTGTGGCCCAAGGATGCTTTTGTATAGACAAACATATGGCTGAGGGTACTTTTAGTGATC	1005

## RESULT 8

US-08-818-581B-3

; Sequence 3, Application US/08818581B

Publication No. US20020007499A1

GENERAL INFORMATION:

APPLICANT: SLABAS, Antoni Ryszard

APPLICANT: BROWN, Adrian Paul

; APPLICANT: BROUGH, Clare Louise

APPLICANT: KROON, Johannes Theodorus Maria

;  
TITLE OF INVENTION: DNA SEQUENCE ENCODING PLANT

TITLE OF INVENTION: 2-ACYLTRANSFERASE

; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:CORRESPONDENCE ADDRESS:  
ADDRESS: COONAR & P

ADDRESSEE: Cooper & Dunham LLP  
STREET: 1195 Avenue of the Americas

STREET: 1185 Avenue of the Americas  
CITY: New York

CITY: New York  
STATE: New York

STATE: NEW YORK  
COUNTRY: US

COUNTRY: US  
ZIP: 10036

COMPUTER READA

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;
; MEDIUM TYPE: Floppy
;

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COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0

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; CURRENT APPLICATION DATA:

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APPROVAL NUMBER: US

; FILING DATE: March 14, 1997

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: NO DCE /

APPLICATION NUMBER: WO PCT/GB96/00306  
FILING DATE: 09 FEB 1996

FILING DATE: 09-FEB-1996  
APPLICATION NUMBER: CP 8

; APPLICATION NUMBER: GB 9502468.3  
 ; FILING DATE: 08-FEB-1995

FILED DATE: 09-FEB-1993



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;
; LENGTH: 1829
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_32632C.1
US-10-437-963-27991

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Query Match          36.8%; Score 550.8; DB 17; Length 1829;
Best Local Similarity 68.8%; Pred. No. 4.3e-134;
Matches 772; Conservative 0; Mismatches 347; Indels 3; Gaps 1;
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QY  
102 GGGCTGGGCTGGGCTGGGCATGGCTATTGCAGCAGCGCCGGTGGTACCATTTG 161

Dh  
1528 GGGCAGGACAGGGCGGAGGGGCCATGGCGGTCCCACCTGTCGTGCTGCTCCCGGTC 1469

QY 162 GGCCGCTCTTCTTCGGCTCCGGCCTCCTTGTTAATCTCATTCAGGCAATATGCTATTC 221  
|||||  
db 1468 GGCCCTCTCTTCTCCTCTCTCCGGCTCATCATCAACGGCATCCAGGCGCTCCTGTTTCTC 1409

222 GTCTAAGCCCGGTGTCGAAAAGTTTGTACAGAAAGGATCAACCGGGTACTAGCAGAGCTC 281

Db	1408	TCGATAAGCCCGTTCTCGAAGAGCTTGTAACGGCGGATCAACAGGTTCTTGGCCGAGCTG	134
Qy	282	TTGTGGCTGGAGCTTGTAATGGCTTATTGATTGGTGGGAGGAGTTAAGGTCCAAATATTC	341

Db 1348 CTGTGGCTTCAGCTGGCTGGCTTGTGGATTGGTGGGCAGGAGTTAAGATACAACCTGCAT 1289

QY  
342 ACAGATCATGAAACCTTTCGTATTAGCGAATAATGACGACGGCCTTTCTGTTTGCCGTTT  
DB  
1288 GCTGATGACGGAACCTTACAAGGCAATGGGAATGAGCATGCACCTTGTCATATCAAATCAT 1229

402 AGAAGTGAATATTGATTGGCTTGTGGATGGGTTTCAGCTCAGCGTTTCAGTTGTCTTGGC 461

1228 CGGAGCGATATCGATTGGCTTATTGGGTGATTTTGGCACAGCGCTCAGGATGCCTTGGG 1169

Qy 462 AGCACTCTAGCTGTGATGAGAAATCTTCAAAGTTTCTGCGGTCATTGGCTGGTCAATG 521

Db	1168	AGTACACITGCTGTTATGAGACAAATCATCGAAATTCCTTCCAGTTATTGGCTGGTCCATG	1109
Qy	522	TGGTTTCTGAGTATCTTTTTCTGGAGAGAAGTTGGGCCAAGGATGAAAGCACATTAAAG	581

Db 1108 TGGTTTGCAGAAATACCTCTTTTGGAAAGGAGCTGGCAAGGATGAAAACACATTGAAA 1049

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Qy 642 GGAACGGCTTTACACAGGCCAAACTATTAGCTGCTCAGGAAATATGCCACTTCCACTGGA 701

db 988 GGCACCTCGCTTTACTCCAGCAAAGCTTCTACGAGCTCAGGAGTATGCTGTTTACACAGGGT 929

Qy 702 TTGCCTGTTCTCTAGAAATGTTTGTGATTCCAAGACTAAGGGTTTTGTTTCTGCAGTAAGT 761

Accession	Sequence	Position
Db	928 TTGCCAGCACCCAGAAATGATTGATTCACGACAAAGGGATTGTATCAGCTGTAAC	869
Qy	762 CATATGCGTCAATTTGTTCTCGCCATTTATGATGTAAACAGTAGCCATCCCTAAGAGTTCC	821

Db  
868 ATTATGGGGGATTTTGTTCACGCTATTTATGATACAACAGCAATTATTCCAAAAGATTCA 809

C:  
922 CCGCCGCCGCACAAATCCGAACACACTTTCAAAGGACACAAACCTTCGCTCCTGGCATCTTCATATC 881

QY  
822 CCTCCTCCATCAAGAGCTCTTTCAGGAGCAATCTTCAGTGGTACATGTCGATG 749

Db  
808 CCTCAACCAACATGCTGCGGATTTTGAAGGCAATCTTCAGTGGTACATGTCGATG 749

Qy  
882 AAGAGGCAATTTCATGAAGAACTGCCAGATACAGATGAGCGTGTTCATCATGGTGTCGA 941

Dp  
748 AAACGTCATGCACAATGAGTCAGATGCCAAAAGTCAGAAGACGATGTTTCAAATAATGGTGCAAA 689

QY 942 GATATATTGTGGCCAAGGATGCTTTGTTAGACAAACATATGSGCTGAGGCTACTTTAGT 1001

Db	688	GACATCTTTGACCAAGGATGCTACTGGATAAGCATTTGGGACAGGCACCTTT	632
Qy	1002	GATCAAGAGTCGAGGATACTGGTCGACCAATAAAGTCTCTTCTGGTAGTTATATCTTGG	1061

[illegible]



Db 536 TTGCGAGTACCTCTTTTGGAGAGGAGCTGGGCCAAGGATGAAAGACACTAAAGTGG 595  
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Db 596 GGTCTCCAAAGGTTGAAAGACTTCCCTAGACCAATTTTGGCTAGCTCTTTTGTAGGGT 655  
QY 645 ACGCGTTTACACAGGCCCAACTATTAGCTGCTCAGGAATATGCCACTTCCACTGGATTG 704  
Db 656 ACTCGTTTACTCCAGCAAGCTTCTCGCAGCTCAGGAGTATGGGGTTCCTCCAGGGCTTA 715  
QY 705 CCTGTTCTAGAAATGTTTGTATTTCCAAAGAACTAAGGTTTGTCTGTCAGTAAGTCAT 764  
Db 716 CCAGCTCTAGAAATGTACTTATTTCCACGTACCAAGGATTTGTATCTGCCGTAAATATT 775  
QY 765 ATGCGCTCATTTGTTCTCCCATTTATGATGTAAACAGTAGCCATCCCTAAGAGTTCCCT 824  
Db 776 ATGCGAGATTTTGTCTCCAGCCATTTACGATACAACTGTAATAGTTCTCTAAGATTCCCT 835  
QY 825 GCTCCTACATGCTAAGACTCTTCAAGGGACAACTTCAAGTGTGCTGCTGCTATCAAG 884  
Db 836 CAACCAACAATGCTCGGATTTTGAAGGGCAATCATCAGTGATACATGTCGCGATGAA 895  
QY 885 AGGCATTGATGAAGGAACTGCCAGATACAGATGAGGCTGTTGCTCAATGGTGTGAGAT 944  
Db 896 CGTCATGCAATGAGTGAGATGCCAATCAGATGATGACGTTTCAAAATGGTGTAAAGAC 955  
QY 945 ATATTGTGGCCAAAGGATGCTTTGTAGACAAACATATGGCTGAGGTAATTTTGTAGTAT 1004  
Db 956 ATTTTGTGACAAAGGATGCTTTACTGACAAACATTTGGCAACAGGCACTTT---CGAT 1012  
QY 1005 CAAGAGCTGCAGGATACCTGGTGCACCAATAAAGTCTCTTCTGTTATATATCTTGGCG 1064  
Db 1013 GAGGAGATTAGACCTATCGGCCCGCCAGTGAATCATTTGCTGGTACCTGTTTGGTGC 1072  
QY 1065 TGTCTGTTGTTGGGGTCTGTAAGTCTCTGCAATGGTCTTCTGTTACTCTCTTCTG 1124  
Db 1073 TGCCTGCTGTTGTTGGTGCATCGAGTTCTTCAAGTGGACGAGCTCCTATCGACATGG 1132  
QY 1125 AAGGTGTTGCATTTTTCAGCTTTTGGTTGGCAGTTGTTACTGCACTTATGCAATTTCTG 1184  
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QY 1185 ATTCATTTCTCAGCTCAGAGCTTCAAAACCGGCCAAG 1223  
Db 1193 GTCATGTTCTCCAGGCTGAGCGATCGAGCTCAGCCAAG 1231

RESULT 12  
US-10-425-114-2048  
; Sequence 2048, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 2048  
; LENGTH: 1220  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700201362\_FLI  
US-10-425-114-2048

Query Match 30.3%; Score 453.6; DB 13; Length 1220;  
Best Local Similarity 70.1%; Pred. No. 1.4e-108;  
Matches 639; Conservative 0; Mismatches 269; Indels 4; Gaps 2;  
QY 312 TGGTGGCAGGAGTTAAGTCCAAATATTCACAGATCATGAAACCTTTGTTTAAATGGT 371  
Db 2 TGGTGGCAGGAGTTAAGTCCAAATATTCACAGATCGGATGAGGAACTTTACCGATCAATGGT 61  
QY 372 AAAGAGCATGCACCTTGTGATAAGCAATCACAGAAGTGATATTGATTGGCTTGTGGATGG 431  
Db 62 AAAGAGCATGCACCTCGTCATATCAAAATCATCGAAGTGATATTGATTGGCTTATTGGATGG 121  
QY 432 GTTTCAGCTCAGCGTTTCAGGTTGTCTTGGCAGCACCTCTAGCTGTGATGAAGAAATCTTCA 491  
Db 122 ATATTGGCCAGCGCTCAGGTTGCCCTTGAAGTACGCTCGCTGTCTATGAAGAAATCATCC 181  
QY 492 AAGTTTCTGCGGTCATTGGCTGGTCAATGTGGTTTCTGAGTATCTTTTCTGGAGAGA 551  
Db 182 AAGTTCTCTCCAGTCAATGGCTGGTCAATGTGGTTTGCAGAGTACCTCTTTTGGAGAGG 241  
QY 552 AGTTGGCCAAAGGATGAAGCACATTAAGTCAAGGATCCAGCGACTGAGTGAATTCCT 611  
Db 242 AGCTGGCCAAAGGATGAAGGACACTAAAGTGGGTTCTCAAAGGTTGAAAGACTTCCCT 301  
QY 612 CTTCCCTTTTGGCTAGCTCTCTTTGTGAAAGGAAACGCGTTTACACAGGCCAAATATTA 671  
Db 302 AGACCAATTTGGCTAGCTCTTTTGTGAGGTTACTCGCTTTTACTCCAGCAAGCTTCTC 361  
QY 672 GCTGCTCAGGAATATGCCACTTCCACTGGATGCTGTTTCTAGAAATGTTTGTGATCCA 731  
Db 362 GCAGCTCAGGAGTATGCGGCTTCCAGGGCTTACCAGCTCCTAGAAATGATCTTATCCA 421  
QY 732 AGAACTAAGGTTTGTGTTCTGCAATAGTCAATGCGCTCATTTGTTCTGCCATTTAT 791  
Db 422 CGTACCAAGGATTTGTATCTGCCGTAAGTATTATCGGAGATTTTGTCCAGCCATTTAC 481  
QY 792 GATGTAACAGTAGCCATCCCTAAGAGTTCCCTGCTCTACAAATGCTAAGACTCTTCAAG 851  
Db 482 GATACAACTGTAATAGTCTTAAAGATTTCCCTCAACCAACAATGCTCGGATTTGAAA 541  
QY 852 GGACAACTTTCAGTGGTGATGTTTCAATATCAAGAGGCAATTTGATGAAGGAACTGCCAGAT 911  
Db 542 GGGCATCATCAGTGATACATGTCCGATGAACGCTCATGCAATGAGTGAATGCCAAA 601  
QY 912 ACAGATGAGGCTGTTGCTCAATGGTGTGAGATATATTTGTGGCCAAAGGATGCTTTGTTA 971  
Db 602 TCAGATGATGACGTTTCAAAAT-GTGTAAGACATTTTGTGGCAAGGATGCTTACTG 660  
QY 972 GACAAACATATGGCTGAGGGTACTTTTAGTGTATCAAGAGCTGCAGGATACTGTTGACCA 1031  
Db 661 GACAAACATTTGGCAACAGGCACTTT---CGATGAGGAGATTAGACCTATCGGCGGCCCA 717  
QY 1032 ATAAAGTCTCTTCTGCTAGTTATATCTTGGCGGTGCTGTTGTTGGGGGTCTGTAAAG 1091  
Db 718 GTGAAATCATTTGCTGCTGACCTGTTTGGTGTGCTGCTCTCTGTTGTTGGTGCATCGAG 777  
QY 1092 TTCTGCAATGGTCTTCTGTTACTCTCTTCTGGAAGGGTGTTCGATTTTTCAGCTTTTGGT 1151  
Db 778 TTCTTCAAGTGGACGAGCTCTCTATCGACATGGAGAGGAGTGGCATTCACCTGCCGAGG 837  
QY 1152 TTGGCAGTTGTTACTGCACTTATGCAAAATTTCTGATTAATTTCTCAGCTCAGAGCTTCA 1211  
Db 838 ATGGGCTCGTGACAGGGCTCATGCAAGTCTTCTCATGTTCTCTCCAGGCTGAGCGGTG 897  
QY 1212 AACCCGCGCAAG 1223  
Db 898 AGCTCAGCCAAG 909

RESULT 13  
US-10-425-114-16071  
; Sequence 16071, Application US/10425114  
; Publication No. US20040034888A1





Db 481 TGGCGAATTAAAGTTGCATTTATGTGTGATGAGTGACTCATGTAATGCTCATTTATTTG 540  
QY 1326 CTTTCAACATCTTATCATAGTATGCTTCTTATTTCTATATATGTAATGTAATGCTTAT 1385  
Db 541 CTTTCAAAATCTTATCATGATGATGTTTCTATTTCTATATATGTAATGTAATGCTTAT 600  
QY 1386 CGATTCAATGTTTTTAATTAAATTAGGATATCCTTTTGTATTGACAGTCTAGGGGATGCC 1445  
Db 601 CGATTCAATGTTTTTAATTAAATTAGGATAT-CTTTTGTATCGACAATCTA--GGATGGC 657  
QY 1446 CTAGAAAAATTCACCCCTATTTTATTTAAAAAATAAAAAAATAAAAAA 1495  
Db 658 CTAGAAAAATTCACCCGCTCTTTTATTTAAAAAATAAAAAAATAAAAAA 707

RESULT 15  
US-10-021-323-14948  
; Sequence 14948, Application US/10021323  
; Publication No. US20040123340A1  
; GENERAL INFORMATION:  
; APPLICANT: Deikman, Jill  
; APPLICANT: Feng, Paul C.C.  
; APPLICANT: Fincher, Karen L.  
; APPLICANT: Ziegler, Todd E.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(52274)B  
; CURRENT APPLICATION NUMBER: US/10/021,323  
; CURRENT FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 60/255, 619  
; PRIOR FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 17880  
; SEQ ID NO 14948  
; LENGTH: 581  
; TYPE: DNA  
; ORGANISM: Gossypium hirsutum  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3829-018-Q6-K6-F2  
US-10-021-323-14948

Query Match 26.0%; Score 388.8; DB 17; Length 581;  
Best Local Similarity 80.5%; Pred. No. 1e-91;  
Matches 467; Conservative 0; Mismatches 112; Indels 1; Gaps 1;  
QY 375 GAGCATGCACTTGTGATAAGCAATCAGAGAGTGATATTGCTTGGATGGGTT 434  
Db 2 GAACATGCCCTTCTCTACCCCAATCAG-AGTGATATTGATTGGTAGTTGGATGGGTT 60  
QY 435 TCAGCTCAGCGTTTCAGGTGTCTTGGCAGCACTCTAGCTGTGATGAAGAAATCTTCAAAG 494  
Db 61 CTGGCTCAGCGATCAGGTGTCTTGGCAGTTCAATAGCTGTGATGAAGAAATCATCAAAA 120  
QY 495 TTTCTGCCGTCATTTGGCTGGTCAATGTGGTTTCTGAGTATCTTTTCTGGAGAGAAGT 554  
Db 121 TTCTCTCCCGTCATAGGTGGTCAATGTGGTTTCTGAGTATCTGTGTTTGGAGAGAGC 180  
QY 555 TGGGCCAAGGATGAAAGCACATTAAGTCAGGCATCCAGCGACTGAGTGATTTCCCTCTT 614  
Db 181 TGGGCCAAGGATGAAACACGATAAAGCAGGCCCTTCAACGTTTAAGGGACTATCCACAG 240  
QY 615 CCCTTTTGGCTAGCTCTCTTTGTAGAAGGAACGCGTTTACACAGGCCAACTATTAGCT 674  
Db 241 CCATTTTGGTTGGCGCTTTTGTAGAAGGAACCTCGCTTACACAGCAAAGCTTGTGCA 300  
QY 675 GCTCAGGAATATGCCACTTCCACTGGATGCCCTGTTCCTAGAAATGTTTGTATCCAAAGA 734  
Db 301 GCTCAGGAATATCGACCTCACAGGATGCTTATACCTATACCTAGAAAGCTTGTATCCCTCGT 360  
QY 735 ACTAAGGGTTTGTCTGTCAGTAAGTCATATCGCTCATTTGTTCTGCCATTATGAT 794  
Db 361 ACAAAGGGTTTGTCTGTCAGTCGTAAGTCATATCGCATCTTTGTCCAGCCATTATGAT 420

QY 795 GTAACAGTAGCCATCCCTAAGAGTTCCTCTGCTCCTAACAATGCTAAGACTCTTCAAGGA 854  
Db 421 ATTACAGTGGCTATTCCCAAAAGCTCACCTTCACTACAATGCTTTAGACTTTTCAAGGG 480  
QY 855 CAACCTTCAGTGGTGCATGTTTCATATCAAGAGGCAATTTGATGAAGGAAGTCCAGATACA 914  
Db 481 CAATCTTCTGTGTACACGTACATATCAAAACGACACCTCATGAAGGAAGTGCCTGAAATG 540  
QY 915 GATGAGGCTGTTGCTCAATGGTGTGCGAGATATATTTGTGG 954  
Db 541 GATGAGGCTGTTGCAACAATGGTGTAAAGATCTGTTTGTGG 580

Search completed: July 9, 2004, 23:03:53  
Job time : 526 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 9, 2004, 18:57:17 ; Search time 2827 Seconds  
(without alignments)  
15823.681 Million cell updates/sec

Title: US-09-914-098-55  
Perfect score: 1498  
Sequence: 1 gcacgaggttcggtttgtg.....aaaaaaaaaaaaaact 1498

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_est3:\*  
12: gb\_est4:\*  
13: gb\_est5:\*  
14: gb\_est6:\*  
15: em\_estom:\*  
16: em\_gss\_hum:\*  
17: em\_gss\_inv:\*  
18: em\_gss\_pln:\*  
19: em\_gss\_vrt:\*  
20: em\_gss\_fun:\*  
21: em\_gss\_mam:\*  
22: em\_gss\_mus:\*  
23: em\_gss\_pro:\*  
24: em\_gss\_rod:\*  
25: em\_gss\_phg:\*  
26: em\_gss\_vrl:\*  
27: gb\_gss1:\*  
28: gb\_gss2:\*  
29: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	602	40.2	602	14	CA819096
2	561	37.4	739	13	BQ123121
3	533.4	35.6	570	12	BI974194
4	531.8	35.5	824	12	BG585493

5	522.8	34.9	1592	11	AY109624	AY109624	Zea mays
6	492.6	32.9	780	12	BG585566	EST487330	BG585566
7	485.8	32.4	739	14	CK240532	VRJ343T7	CK240532
8	476.8	31.8	763	12	BG585567	EST487331	BG585567
9	468	31.2	564	12	BM523947	sal05e03	BM523947
10	465.4	31.1	620	10	AW508939	si38b11.y	AW508939
11	463.2	30.9	692	14	CA900082	PCSC21606	CA900082
12	461.2	30.8	656	10	AW695931	NF100G06S	AW695931
13	442.8	29.6	466	14	CD400176	Gm_ck2194	CD400176
14	436.4	29.1	670	14	CB970126	CAB10003	CB970126
15	434.4	29.0	685	13	BQ403131	GA_Ed005	BQ403131
16	432.4	28.9	698	14	CF210882	CAB20007	CF210882
17	429.6	28.7	649	10	AW773846	EST332832	AW773846
18	427.4	28.5	882	10	BF268651	GA_EB000	BF268651
19	418.8	28.0	814	14	CD820693	BN20_0531	CD820693
20	415.6	27.7	557	14	CA936841	sav25c01	CA936841
21	413.4	27.6	763	14	CF672320	RTCNT1_62	CF672320
22	405.6	27.1	564	12	BM892810	sam64f01	BM892810
23	401.2	26.8	746	14	CD836813	BN45_049P	CD836813
24	400	26.7	672	14	CB074283	EST00795	CB074283
25	399.2	26.6	745	14	CF437515	EST673860	CF437515
26	395.6	26.4	490	10	AW620973	sj98e03.y	AW620973
27	389.8	26.0	542	14	CA785831	sat39h01	CA785831
28	387.2	25.8	676	14	CD826229	BN25_063C	CD826229
29	381	25.4	829	14	CB654545	OSJNEC07C	CB654545
30	381	25.4	850	14	CB644085	OSJNEB05C	CB644085
31	377.6	25.2	666	14	CD820168	BN20_051G	CD820168
32	371.6	24.8	498	10	BF637273	NF047D10L	BF637273
33	370.8	24.8	560	12	BI405683	048D08_Ma	BI405683
34	370.8	24.8	667	14	CD831577	BN40_060B	CD831577
35	370.2	24.7	840	14	CB620801	OSIIEa06D	CB620801
36	369	24.6	701	12	BJ463828	BJ463828	BJ463828
37	367.8	24.6	545	14	CA900078	PCSC09348	CA900078
38	367.8	24.6	833	14	CB644127	OSJNEB05D	CB644127
39	367.4	24.5	695	13	BQ764802	EBca01_SQ	BQ764802
40	365.4	24.4	765	14	CD437887	EL01N0506	CD437887
41	365.4	24.4	866	14	CK152069	FGAS03496	CK152069
42	360.2	24.0	397	12	BM308598	sak48b08	BM308598
43	359	24.0	636	13	BU879456	V060D12_P	BU879456
44	354.2	23.6	776	14	CB682848	OSJNEF10J	CB682848
45	351.2	23.4	614	12	BG356169	EM1_22_C1	BG356169

ALIGNMENTS

RESULT 1  
CA819096  
LOCUS  
DEFINITION  
CA819096 602 bp mRNA linear EST 09-DEC-2002  
sau68h05.y1 Gm-cl071 Glycine max cDNA clone SOYBEAN CLONE ID:  
Gm-cl071-6130 5' similar to TR:Q9SDN3 Q9SDN3  
1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE. ; mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
CA819096  
EST.  
Glycine max (soybean)  
Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
1 (bases 1 to 602)  
Shoenaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.  
Public Soybean EST Project  
Unpublished (1999)  
Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine



Db 1 ACATTGATTGGCTTTTCGGATGGATTTTAGCTCAGCGTTCCAGGATGCCTTGGTAGCAGCG 60

Qy 469 TAGCTGTG-ATGAAGAAATCTTCAAAGTTTCTGCCGTCATTTGGTGTCAATGTGTTT 527

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Qy 588 ATCCAGCGACTGAGTATTCCTCTTCCCTTTTGGCPAGCTCTCTTTGTAGAGGAACG 647

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Db 237 CGCTTTACAGGCCAAATATTAGCCGCTCAGGAATATGCAACCTCAACTGGATTGCCT 296

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Db 297 GTTCCTAGAAACGTTTGTATCCAGAACTAAGGTTTTTGTCTGCAAGTAAGTCATATG 356

Qy 768 CGCTCATTTGTTCCCTGCAATTTATGATGTAACAGTAGGCATCCCTAAGATTTCCCTGCT 827

Db 357 CGCTCATTTGTTCCAGCCATTTATGATGTAACAGTAGGCATCCCTAAGATTTCCCTGCT 416

Qy 828 CCTACAAATGTAAGACTCTTCAAGGCAACCTTCAGTGGTGCATGTTTCATATCAAGAG 887

Db 417 CCTACAAATGTAAGACTCTTCAAGGCAACCTTCAGTGGTGCATGTTTCATATCAAGAG 476

Qy 888 CATTTGATGAAGAACTGCCAGATACAGATGAGGCTGTTGCTCAATGGTGTGAGATATA 947

Db 477 CATTTGATGAAGATTTGCCAGAGCAGAGGAAGCTGTTGCTCAATGGTGTGAGACATA 536

Qy 948 TTTGTGGCCAGGATGCTTTGTTAGACAAACATATGGCTGAGGTTACTTTAGTGATCAA 1007

Db 537 TTTGTGGCTAAGGATGCTTTGTTAGACAAACATATGCTGATGACAAATTCAGTGATCAC 596

Qy 1008 GAGCTGCAGGATACTGGTCGACCAATAAAGTCTCTTCTGCTAGTTATATCTTGGGCGTGT 1067

Db 597 GAGCCACGGATCTTGGTCGACCAATAAAGTCTCTTCTGCTAGTTATATCAATGGATTGT 656

Qy 1068 CTGGTTGTTGGGGTCTGTAAAGTTCCCTGCAATGTTCTGTTACTCTTCTCTGGAAG 1127

Db 657 GTCGTCGTTGGGGACTGTTAAGTTGCTTCAATGTTCTTCACTACTATCTCTTGGAG 716

Qy 1128 GGTGTTGCATTTTCAGCTTTTGG 1150

Db 717 GGTGTTGCATTTTCAGTATTTAG 739

RESULT 3

BI974194

LOCUS

DEFINITION

sai97g03.y1 Gm-cl065 Glycine max cdna clone GENOME SYSTEMS CLONE

ID: Gm-cl065-9125 5', similar to TR:Q9XFW4 Q9XFW4

ACYL-COA:1-ACYLGLYCEROL-3-PHOSPHATE ACYLTRANSFERASE ;, mRNA

sequence.

ACCESSION

BI974194

VERSION

BI974194.1 GI:16348599

KEYWORDS

EST.

SOURCE

Glycine max (soybean)

ORGANISM

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE

1 (bases 1 to 570)

AUTHORS

Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,

McCann, R., Waterston, R. and Wilson, R.

Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com

High quality sequence stop: 422.

FEATURES

Source

Location/Qualifiers

1..570

/organism="Glycine max"

/mol\_type="mRNA"

/db\_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-cl065-9125"

/tissue\_type="germinating shoots"

/lab\_host="DH10B"

/clone\_lib="Gm-cl065"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from germinating shoots of the cultivar Williams. The seeds were allowed to germinate for 24 hours prior to being cold stressed for 2 days at 4C. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

ORIGIN

Query Match 35.6%; Score 533.4; DB 12; Length 570;

Best Local Similarity 99.8%; Pred. No. 8.7e-82;

Matches 534; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GAGGTTCCGTTTGTGCTGACCTGACCTCGGAAATCCAAAGAGGAAACTCACGGTGTTCGT 64

Db 36 GTGGTTCCGTTTGTGCTGACCTGACCTCGGAAATCCAAAGAGGAAACTCACGGTGTTCGT 95

Qy 65 TCGTGTGTCTGTCTGTCT 124

Db 96 TCGTGTGTCTGTCTGTCT 155

Qy 125 CATGGCTATTGCAGCAGCGCGCGTGGTGGTACCATTTGGGCGCTGCTCTCTCTCGCCTCCGG 184

Db 156 CATGGCTATTGCAGCAGCGCGCGTGGTGGTACCATTTGGGCGCTGCTCTCTCTCGCCTCCGG 215

Qy 185 CCTCCTTGTAAATCTCATTCAGGCAATATGCTATGTCGTAAGGCCGGTGTGCGAAAAG 244

Db 216 CCTCCTTGTAAATCTCATTCAGGCAATATGCTATGTCGTAAGGCCGGTGTGCGAAAAG 275

Qy 245 TTGTACAGAGGATCAACCGGCTAGTAGCAGAGCTCTTGTGGCTGGAGCTTGTATGGCT 304

Db 276 TTGTACAGAGGATCAACCGGCTAGTAGCAGAGCTCTTGTGGCTGGAGCTTGTATGGCT 335

Qy 305 TATTGATTGGTGGCAGGAGTTAAGGTCCAAATATTACAGATCATGAAACCTTTCGTTT 364

Db 336 TATTGATTGGTGGCAGGAGTTAAGGTCCAAATATTACAGATCATGAAACCTTTCGTTT 395

Qy 365 AATGGGTAAAGACATGCACITTTGTGATAAGCAATCACAGAGTATATTGATTGGCTTGT 424

Db 396 AATGGGTAAAGACATGCACITTTGTGATAAGCAATCACAGAGTATATTGATTGGCTTGT 455

Qy 425 TGGATGGGTTTCAGCTCAGCGTTTCAGGTTGTCTTGGCAGCCTCTAGCTGTGATGAAGAA 484





/db\_xref="MaizeDB:630905"  
/db\_xref="taxon:4577"  
/clone\_lib="Maize Mapping Project/DuPont Cornsensus Library"  
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Query Match 34.9%; Score 522.8; DB 11; Length 1592;  
Best Local Similarity 65.7%; Pred. No. 3.6e-80;  
Matches 720; Conservative 0; Mismatches 373; Indels 3; Gaps 1;

QY	128	GGCTATTGCAGCAGCGCGCGTGGTGGTACCATTTGGCCCTGCTCTTCTTCGCTCCGGCCT	187
Db	214	GGCGATCCCGCTCGTCTCGTGGTCTCCCGCTCGGCTGCTCTTCTTCCTGCTCCGGCCT	273
QY	188	CCTTGTAAATCTCATTCAGGCAATATGCTATGTCGTGTAAGCCGGTGTGCAAAAGTTT	247
Db	274	CATCGTCAACACCATCCAGGCCATCTATTGTGACAATAAGGCCCTTTTCCAAGAGCTT	333
QY	248	GTACAGAAGGATCAACCGGCTAGTAGCAGAGCTCTTGTGGCTGGAGCTTGATGGCTTAT	307
Db	334	GTATCGCCGATCAACAGGTTCTTTGGCCGAGCTGCTGTGGCTCCAGCTTGTCTGGTGGT	393
QY	308	TGATTGGTGGCAGGAGTTAAGGTCCAAATATTACAGATCATGAAACCTTTCGTTTAAAT	367
Db	394	GGACTGTGGCAGGCGTTAAGGTACAACCTGCATGCGGATGAGGAACTTACCGATCAAT	453
QY	368	GGGTAAGAGCATGCACCTTGTGATAAGCAATCAACAGATCATGAAACCTTTCGTTTAAAT	427
Db	454	GGGTAAGAGCATGCCCTCGTCATATCAAAATCATCGAAGTATATTGATGGCTTATTGG	513
QY	428	ATGGGTTTCAGCTCAGCGTTTCAGGTTGTCTTGGCAGCACTCTAGCTGTGATGAAGAAATC	487
Db	514	ATGGATATTGGCCCGCAGCGCTCAGGGTGCCCTTGAAGTACACTCGCTGTGATGAAGAATC	573
QY	488	TTCAAAGTTTTCGCGGTCACTGGCTGGTCAATGTGTTTCTGAGTATCTTTTCTCGGA	547
Db	574	ATCCAAGTTTCTTCCAGTTATTTGGTGTGTTGTTTGCAGAGTACCTCCTNNNNNGA	633
QY	548	GAGAAAGTTGGCCCAAGGATGAAAGCACATTTAAAGTCAGGCATCCAGCGACTGAGTGATT	607
Db	634	AAGGAGCTGGGCCAAGGATGAAAGACACTAAAGTGGGTCTCCAAGGTTGAAAGACTT	693
QY	608	CCCTCTTCCCTTTTGGCTAGCTCTCTTTGTGAGAAGGAACCGTTTTTACAGGCCCAACT	667
Db	694	CCCTAGACCAATTTTGGCTAGCTCTTTTCGTCGAGGGTACTCGCTTTACTCCAGCAAGCT	753
QY	668	ATTAGCTGCTCAGGAATATGCCACTTCCACTGGATTGCTGTTCTCTAGAAATGTTTTCAT	727
Db	754	TCTCGCAGCTCAGGAATATGCGGCCCTCCAGGGCTTACCAGGCTCCTAGAAATGTACTTAT	813
QY	728	TCCAAGAACTAAGGGTTTGTCTGCAAGTATCATATGCGCTCATTTGTTCTCGCCAT	787
Db	814	TCCACGTACCAAGGGATTGTATCTGCTGTAAGTATTATCGGAGATTTTGTTCAGCCAT	873
QY	788	TTATGATGTAAACAGTAGCCATCCCTAAGATTCCCTGCTCCTACAAATGCTAAGACTCTT	847
Db	874	TTATGATACAACTGTAAATAGTCCCTAAAGATTCCCTCAACCAACAATGCTCGGATTTT	933
QY	848	CAAGGGACAACCTTCAGTGGTGCATGTTTCATATCAAGAGGCATTTGATGAAGGAATGCC	907
Db	934	GAAAGGGCAATCATCAGTGATACATGTCCGCATGAACGTCATGCAATGATGAGATGCC	993
QY	908	AGATACAGATGAGGCTGTTCTCAATGGTGTGAGATATATTGTGGCCAAAGGATGCTTT	967
Db	994	AAAATCAGATGAGGATGTTTCAAAATGGTGAAGACANNANNGTGGCAAGGATGCCCTT	1053
QY	968	GTTAGACAAACATATGGCTCAGGGTACTTTTAGTGATCAAGAGCTGCAGGATACCTGGTCG	1027

Db	1054	ACTGACAAGCATTTGGCAACAGGCACCTTT---CGATGAGGAGATTAGACCTATTGGCCG	1110
QY	1028	ACCAATAAAGTCTCTTCTGGTAGTTATATCTTGGCGTGTCTGCTGTTGTCGGGCTCTGT	1087
Db	1111	TCCAGTGAAATCATTTGCTGGTGACCCCTGTTCTGCTGCTGCTCTGCTGTTTGGCGCCAT	1170
QY	1088	AAAGTCTCTGCAATGGTCTTCGTTACTCTCTCTCTGGAAGGGTGTTCATTTTTCAGCTTT	1147
Db	1171	CGAGTCTTCAAGTGGACACAGCTTCTGTGACGCTGGAGGGTGTGNNNNNNNNNNNN	1230
QY	1148	TGGTTTGGCAGTTGTTACTGCACCTATGCAAAATCTGATTCAATTCTCACAGTCAGAGCG	1207
Db	1231	NN	1290
QY	1208	TTCAAACCCCGCCAAAG 1223	
Db	1291	GTCGAGCTCAGCCAGG 1306	

RESULT 6  
BG585566  
LOCUS  
DEFINITION  
EST487330 MHAM Medicago truncatula/Glomus versiforme mixed EST  
library cDNA clone pMHAM-3018 5' end, mRNA sequence.  
ACCESSION  
BG585566  
VERSION  
BG585566.1 GI:13600630  
KEYWORDS  
SOURCE  
Medicago truncatula/Glomus versiforme mixed EST library  
ORGANISM  
Medicago truncatula/Glomus versiforme mixed EST library  
Eukaryota; mixed EST libraries.  
REFERENCE  
1 (bases 1 to 780)  
Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Utterback,T., Cho,J.  
and Fraser,C.M.  
ESTs from roots of Medicago truncatula after colonization with  
Glomus versiforme, 2001  
UNPUBLISHED (2001)  
CONTACT: Harrison M.J.  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73401  
Tel: 580-223-5810  
Fax: 580-221-7380  
Email: mjharrison@noble.org  
Noble EST name: N381040e TIGR sequence name: MTDCF52TK More  
information is available at: http://www.medicago.org  
Seq primer: SKmod (CTA GAA CTA gtg gat CC).

FEATURES  
Location/Qualifiers  
1..780  
/organism="Medicago truncatula/Glomus versiforme mixed EST  
library"  
/mol\_type="mRNA"  
/cultivar="Medicago truncatula genotype A17"  
/db\_xref="taxon:119092"  
/clone="pMHAM-3018"  
/tissue\_type="roots colonized with Glomus versiforme"  
/dev\_stage="Roots harvested at 10, 17, 22, 31 and 38 days  
post-inoculation with Glomus versiforme. The library was  
made from a mixture of RNA from each of these stages."  
/lab\_host="E. coli strain XL0LR"  
/clone\_lib="MHAM"  
/note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2:  
XhoI; cDNA was prepared from polyA+ enriched RNA from  
roots harvested at 10, 17, 22, 31 and 38 days  
post-inoculation with Glomus versiforme. The cDNA was  
directionally ligated into the Unizap XR vector from  
Stratagene and packaged using Gigapack III Gold packaging  
extracts. Plasmids containing cDNA inserts were excised  
from the recombinant lambda-Zap phage using Ex-assist  
helper phage and propagated in XL0LR cells."

ORIGIN  
Query Match 32.9%; Score 492.6; DB 12; Length 780;



Db 721 CCTCATCAATTCTCTCA 738

RESULT 8  
BG585567  
LOCUS  
DEFINITION  
Library cDNA clone pMHAM-30110 5' end, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source  
1. 763  
/organism="Medicago truncatula/Glomsu versiforme mixed EST  
library"  
/mol\_type="mRNA"  
/cultivar="Medicago truncatula genotype A17"  
/db\_xref="taxon:119092"  
/clone="pMHAM-30110"  
/tissue\_type="roots colonized with Glomsu versiforme"  
/dev\_stage="Roots harvested at 10, 17, 22, 31 and 38 days  
post-inoculation with Glomsu versiforme. The library was  
made from a mixture of RNA from each of these stages."  
/lab\_host="E. coli strain XL0LR"  
/clone\_lib="MHAM"  
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:  
XhoI; cDNA was prepared from polyA+ enriched RNA from  
roots harvested at 10, 17, 22, 31 and 38 days  
post-inoculation with Glomsu versiforme. The cDNA was  
directionally ligated into the Unizap XR vector from  
Stratagene and packaged using Gigapack III Gold packaging  
extracts. Plasmids containing cDNA inserts were excised  
from the recombinant lambda-Zap phage using Ex-assist  
helper phage and propagated in XL0LR cells."

ORIGIN  
Query Match 31.8%; Score 476.8; DB 12; Length 763;  
Best Local Similarity 86.6%; Pred. No. 3.9e-72;  
Matches 537; Conservative 0; Mismatches 82; Indels 1; Gaps 1;

QY 108 GGCTGGGCTGGGCTGGGCTATTGACAGAGCGGCCGCTGGTACCATTTGGGCTG 167  
Db 144 GACAGAGAGAGGCGGCCATGGCTATTGACAGCGGCTGCTGCTGCTGCTGCTG 203

QY 168 CTCCTTCTTCGCTCCGGCTCGCTGTTAATCTCATTACGCAATATGCTGCTGCTG 227  
Db 204 CTCCTTCTTCGCTCCGGCTCGCTGTTAATCTTTCAGGCAATATGCTGCTGCTG 263

QY 228 AGGCCGGTGTGCAAAAAGTTTGTACAGAGGATCAACCGGCTAGTAGCAGCTCTTGTGG 287  
Db 264 AGACCGCTGTCAAGAAGATTTGTACAGAGGATCAACCGGCTGGTGGCAGAACTGTTGTGG 323

QY 288 CTGGAGCTTGTATGGCTTATTCATTTGGTGGCAGGAGTTAAGGTCCTCAATATTCACAGAT 347

Db 324 CTGGAACCTTTGTTGGCTTATTGATTGGTGGGCTGGAGTTAAGTTGAAATATACACGGAC 383

QY 348 CATGAAACCTTTTCGTTTAATGGGTAAGAGACATGCACCTGTGATAAGCAATACAGAAAGT 407  
Db 384 CGTGAAACCTTCTCGTTTGTATGGGTAAGAAACATGCACCTGTGCATATGCAATACAGAAAGT 443

QY 408 GATATTGATTGGCTTGTGGATGGGTTTCAGCTCAGCGTTTCAGGTTGCTTGGCAGCACT 467  
Db 444 GATATTGATTGGCTTGTGGATGGGTTTGTAGCTCAGCGTTTCGGGTTGCCTTGGCAGTACT 503

QY 468 CTAGCTGTGATGAAGAAATCTTCAAAGTTTCTGCCGGTCAATGGCTGGTCAATGTGGTTT 527  
Db 504 CTAGCAGTGAAGAAATCGTCAAAGTTTCTACCGGTAATGGTGGTCAATGTGGTTT 563

QY 528 TCTGAGTAICTTTTCTGGAGAGAAAGTTGGGCCAAGGATGAAAGCACATTAAAGTCAGGC 587  
Db 564 TCTGAGTAICTTTTCTGGAGAGAAAGTTGGGCCAAGGATGAAAGCACATTGAAATCAGGT 623

QY 588 AT-CCAGCGACTGAGTGAATTTCCCTCTTCCCTTTTGGCTAGCTCTCTTTGTAGAAGAAC 646  
Db 624 ATACCGGCGGTTGAATGAATTTCCCTCTTCCCTTTTGGTGGCTCTCTTTGTAGAAGAAC 683

QY 647 GCGTTTTACACAGGCCAAACTATTAGCTGCTCAGGAATATGCCACTTCCACTGGATTGCC 706  
Db 684 ACGTTTCACAAATGTCAAATATTATTAGCTGCTCAAGAATATGCAACCTCCACTGGATTGCC 743

QY 707 TGTTCTCTAGAAATGTTTGA 726

Db 744 TGTTCCCTAGAAATGCTTTGA 763

RESULT 9  
BM523947  
LOCUS  
DEFINITION  
sal05e03.y1 Gm-cl057 Glycine max cDNA clone SOYBEAN CLONE ID:  
Gm-cl057-4422 5' similar to TR:Q9SDN3 Q9SDN3  
1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE. ; mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BM523947 564 bp mRNA linear EST 19-FEB-2002  
Glycine max (soybean)  
Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.  
1 (bases 1 to 564)  
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,  
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,  
Beck,C., Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,  
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,  
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
McCann,R., Waterston,R. and Wilson,R.  
Public Soybean EST Project  
Unpublished (1999)  
Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available through: ResGen, Invitrogen Corp. 2130  
South Memorial Parkway Huntsville, AL 35801 For further information  
call: (800)-533-4363 or contact: ccu@resgen.com web site:  
www.resgen.com  
Seq primer: -40R from Gibco  
High quality sequence stop: 414.  
Location/Qualifiers  
1. 564  
/organism="Glycine max"  
/mol\_type="mRNA"  
/db\_xref="taxon:3847"

FEATURES  
source  
1. 564  
/organism="Glycine max"  
/mol\_type="mRNA"  
/db\_xref="taxon:3847"

/clone="SOYBEAN CLONE ID: Gm-c1057-4422"  
/tissue\_type="Degenerating cotyledons, 2 week old seedling"  
/lab\_host="DH10B"  
/clone\_lib="Gm-c1057"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from degenerating cotyledons of 2 week old seedlings from P1468916. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

ORIGIN

Query Match 31.2%; Score 468; DB 12; Length 564;  
Best Local Similarity 89.4%; Pred. No. 1.4e-70;  
Matches 504; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 450 GGTGTTCTGGCAGCACCTCTAGCTGTGATGAAGAAATCTTCAAAAGTTTCTGCCGTCATT 509  
Db 1 GGTGTTCTGGCAGCACCTCTAGCTGTGATGAAGAAATCTTCAAAAGTTTCTGCCGTCATT 60  
QY 510 GGCTGTCATATGTTGTTTCTGAGTATCTTTTCTGGAGAGAAGTTGGGCCAAGGATGAA 569  
Db 61 GGTGTTCTGATGTTGTTTCTGATATCTTTTCTGGAGAGAAGTTGGGCCAAGGATGAA 120  
QY 570 AGCACATTAAGTTCAGGCATCCAGCGACTGAGTGAATTCCTCTCTTCCCTTTTGGCTAGCT 629  
Db 121 CGCACATTAAGTTCAGGCATCCAGCGACTGAGGGAATTCCTCTCTTCCCTTTTGGCTAGCT 180  
QY 630 CTCTTTGTAAGGAACCGGTTTACACAGGCCAACTATTAGTGTCTCAGGAATATGCC 689  
Db 181 CTCTTTGTAAGGAACCGGTTTACACAGGCCAACTATTAGTGTCTCAGGAATATGCC 240  
QY 690 ACTTCCACTGATGCTGCTTCTTCAAGAAATGTTTGAATCCAAAGAACTAAGGGTTTGT 749  
Db 241 GCCTCAGTGGATGCTGCTTCTTCAAGAAATGTTTGAATCCAAAGAACTAAGGGTTTGT 300  
QY 750 TCTGCAGTAAGTCATATCGGCTCATTTGTTCTGCAATTTATGATGTAACAGTAGCCATC 809  
Db 301 TCAGCAGTAAGTAACCATATCGGCTCGTTTCTGCTGCAATTTATGATGTAACAGTAGCCATC 360  
QY 810 CCTAAGAGTCCCTGCTCCTACATGCTAAGACTCTTCAAGGGACAACCTTCAAGTGGTG 869  
Db 361 CCCAAGAGTCCCTGCTCCTACATGCTAAGACTCTTCAAGGGACAACCTTCAAGTGGTG 420  
QY 870 CATGTTTCATATCAAGAGGCATTTGATGAAGAACTGCGCATATCAGATGAGCTGTGCT 929  
Db 421 CATGTCATATTAAGCGGCATGCGATGAAGGATTTGCCAGAGAAGATGAAGCTGTGCT 480  
QY 930 CAATGGTTCGAGATATATTTGTTGGCCAAGGATGCTTTGTTAGACAAACATATGCTGAG 989  
Db 481 CAATGGTTCGAGATGTTTGTGGCTAAGATGCAATGTTGTTAGACAAACATATGCTGAG 540  
QY 990 GGTACTTTTAGTATCAAGAGCTG 1013  
Db 541 GACACATTTAGTATCAAGAGCTG 564

RESULT 10  
AW508939  
LOCUS

DEFINITION  
si38b11.y1 Gm-r1030 Glycine max cDNA clone linear EST 03-DEC-2001  
Gm-r1030-1174 5' similar to TR:Q40119 Q40119  
1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE ;, mRNA sequence.

ACCESSION  
AW508939  
VERSION  
AW508939.1 GI:7147017  
KEYWORDS  
EST.

SOURCE  
ORGANISM

Glycine max (soybean)  
Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.

REFERENCE  
AUTHORS

1 (bases 1 to 620)  
Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V.,  
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,  
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,  
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,  
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
McCann, R., Waterston, R. and Wilson, R.

TITLE  
JOURNAL  
COMMENT

Public Soybean EST Project  
Unpublished (1999)  
Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130  
South Memorial Parkway Huntville, AL 35801 For further information  
call: (800)-533-4363 or contact via email: ccu@resgen.com  
High quality sequence stop: 325.

FEATURES

Location/Qualifiers  
1..620  
/organism="Glycine max"  
/mol\_type="mRNA"  
/db\_xref="taxon:3847"  
/clone="GENOME SYSTEMS CLONE ID: Gm-r1030-1174"  
/lab\_host="DH10B"  
/clone\_lib="Gm-r1030"

/note="Vector: pSPORT1; Site 1: Sall; Site 2: NotI; This  
cDNA library was constructed from mRNA isolated from  
immature cotyledons of greenhouse grown plants  
(individual seed fresh weight of 100-300mg). The library  
was prepared using the Life Technologies pSuperScript cDNA  
library construction kit. Complementary DNA was  
synthesized from mRNA using a poly(dT) sequence with a  
NotI restriction site. Sall linkers adapters were ligated  
to the blunt-ended cDNA fragments followed by NotI  
digestion. The cDNA fragments were directionally cloned  
into the NotI-Sall restriction site of the pSPORT1  
vector. The ligated cDNA fragments were transformed into  
E. coli ElectroMax DH10B host cells. This library was  
constructed by Dr. Lila Vodkin and Dr. Anu Khanna. Note  
that Gm-r1030 is a re-rack of Gm-cl007."

ORIGIN

Query Match 31.1%; Score 465.4; DB 10; Length 620;  
Best Local Similarity 86.2%; Pred. No. 3.9e-70;  
Matches 514; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 139 CAGGCGCGTGGTGATGCTATGTCGTAAGCGCGTCTCTCTTCGCTCCGCGCTCCTTGTAAATC 198  
Db 25 CTGCAGTTGTTGTTCTCCCATTTGGGCTTCTCTCTTCGTTCCGCGCTCATCGTTAAAC 84  
QY 199 TCATTCAGGCAATATGCTATGTCGTAAGCGCGTGTGCGGCGTGTGCGGCGGATCTGTACCGCGGA 258  
Db 85 TCATTCAGGCAATATGCTATGTCGTAAGCGCGTGTGCGGCGGATCTGTACCGCGGA 144  
QY 259 TCACCGCGGTAGTACGAGCTCTTGTGGCTGAGCTTGTATGGCTTATTGATGGTGGG 318  
Db 145 TGAACAGGGTGGTGGCGGAGCTGCTCTGGCTGGAGCTCGTGTGGATTTATTGATGGTGGG 204  
QY 319 CAGGAGTTAAGTCCAAATATTACAGATCATGAAACCTTTTCGTTTAAATGGGTAAGAGC 378  
Db 205 CCGTGTTAAGTTCAAGTATTACAGATCTCTGAAACCTTTTCGTTTAAATGGGTAAGAGC 264  
QY 379 ATGCACTTGTGATAAGCAATCAAGAGCTGATATTGCTTGGCTTGTGGATGGTTTCAG 438

Db 265 ATGCTCTTGTATCTCCAAATCACAGAAAGTGACATTGATTGGCTTGTGGATGGGTTTAG 324

QY 439 CTCAGCGTTTCAGGTTGTCTTGGCAGCACTCTAGCTGTGATGAAGAAATCTTCAAAGTTTC 498

Db 325 CTCAGCGTTTCAGGTTGCCTTGGCAGCACTCTTGTCTGTGATGAAGAAATCATCGAAGTTTC 384

QY 499 TGCCGGTCATTGGCTGGTCAATGTGGTTTCTGAGTATCTTTTCTGGAGAGAAAGTTGGG 558

Db 385 TACCGGTCATTGGTTGGTCAATGTGGTTTCTGAGTATCTNTTCTTGGAGAGAAAGTTGGG 444

QY 559 CCAAGGATGAAAGCACATTAAAGTCAGGCATCCAGCACTGAGTGATTTCCTCTTCCCT 618

Db 445 CCAAGGATGAACGCACATTAAATCATGCTTACAGCAACTGAAGGATTTCCTCTTATCT 504

QY 619 TTTGGCTAGCTCTCTTGTGAAGGAACGGGTTTACACAGGCCAAACTATTAGCTGCTC 678

Db 505 TATGGATGGCTCTCTGTGTGAAGGAACCTCGCTGTACACAGGGCCAACTATTAGCTGCTC 564

QY 679 AGGAATATGCCACTTCCACTGGATTGCTGTCTCTAGAAATGTTTGTGATCCAAAGA 734

Db 565 AGGAGTATGACGCTCAGCTAGATTGCCGTGTTCTAGAAATGATTGATCCAAAGA 620

RESULT 11

CA900082

LOCUS

DEFINITION

PCSC21606 Scarlet Runner Bean Suspensor Region TripleX2 Phaseolus coccineus cDNA 5' similar to Acyl-CoA:1-acylglycerol-3-phosphate acyltransferase, mRNA sequence.

ACCESSION

CA900082

VERSION

CA900082.1 GI:27387074

KEYWORDS

EST.

SOURCE

Phaseolus coccineus

ORGANISM

Phaseolus coccineus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.

REFERENCE

1 (bases 1 to 692)

AUTHORS

Bui,A.Q., Le,B.H., Weterings,K., Bi,Y.-P., Choi,J.-S., McElroy,K.E., Choi,P.S., Harada,J.J., Fischer,R.L. and Goldberg,R.B.

TITLE

Gene Activity in Different Regions of a Post-Fertilization Plant Embryo by EST Analysis

JOURNAL

Unpublished (2002)

COMMENT

Contact: Goldberg, R.B.

Department of Molecular, Cell, & Developmental Biology

University of California, Los Angeles

621 Charles E. Young Drive South, Los Angeles, CA 90095-1606, USA

Tel: 310 825 3270

Fax: 310 825 8201

Email: bobg@ucla.edu

Seq primer: 5' TripleX

POLYA=No.

FEATURES

source

1..692

/organism="Phaseolus coccineus"

/mol\_type="mRNA"

/cultivar="Hammond's Dwarf Scarlet"

/db\_xref="taxon:3886"

/dev\_stage="6-days post-pollination"

/clone\_lib="Scarlet Runner Bean Suspensor Region TripleX2"

/note="Organ: Suspensor Region of Globular-Stage Embryos; Vector: TripleX2; Site\_1: SfiIA; Site\_2: SfiIB; Suspensor regions were micro-dissected from globular-stage embryos six days after pollination from greenhouse-grown plants [Weterings et al., Plant Cell 13, 2409-2425 (2001)]. Double-stranded cDNA was synthesized from suspensor mRNA using the SMART cDNA Library Construction Kit according to the manufacturer (Clontech). The suspensor cDNA fragments were directionally ligated into the SfiI restriction site of the lambda TripleX2 vector (Clontech), and the recombinant cDNAs were transformed into E. coli XL1-Blue

cells (Clontech). Suspensor cDNA plasmids used for directional sequencing were obtained by in vivo excision from the lambda TripleX2 recombinants in E. coli BM25.8 cells (Clontech)."

ORIGIN

Query Match 30.9%; Score 463.2; DB 14; Length 692;

Best Local Similarity 86.7%; Pred. No. 8.8e-70;

Matches 510; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 139 CAGCGCCGTTGGTGGTACCAATTTGGGCCCTGCTTCTTTCGCTCCGGCCTCCTTGTAAATC 198

Db 105 CTGAGCTGTTGTGCTTCCACTGGGCCCTTCTCTTCTTCTCCTCTGGCCTCATCGTTAACC 164

QY 199 TCATTTCAGGCAATATGCTATGTCGTCTGTAAGGCCGGTGTGCGAAAGTTTGTACAGAAAGA 258

Db 165 TCATTTCAGGCACTATGCTACGTGTTTGTGCGGCCGGTGTGCGAAGAAATTTGTACCGCGGA 224

QY 259 TCAACCGGGTAGTAGCAGAGCTTCTTGTGGCTGGAGCTTGTATGGCTTATTGATTTGGTGGG 318

Db 225 TGAACCGGGTGTGGCGGAACCTGTTTGTGGTGGAACTCGTGTGGATTATTGATTTGGTGGG 284

QY 319 CAGGAGTTAAGTCCAAATATTCACAGATCATGAAACCTTTCGTTTAATGGGTAAGAGC 378

Db 285 CTGCTGTTAAGGTCCAAATATTCACAGATAGTGAACCTTTTCCTTCAATGGGTAAGAGC 344

QY 379 ATGCACTTGTGATAAGCAATACAGAAAGTGATATTGATTGGCTTGTGGATGGGTTTCAG 438

Db 345 ATGCTCTTGTCTATATCCAAATACAGAAAGTGACATTGATTGGCTTGTGGATGGGTTTAG 404

QY 439 CTCAGCGTTTCAGGTTGCTTTGGCAGCACTCTAGCTGTGATGAAGAAATCTTCAAAGTTTC 498

Db 405 CTCAGCGTTTCAGGTTGCCCTTGGGAGCACTCTAGCTGTGATGAAGAAATCTCTAAGTTTC 464

QY 499 TGCCGGTCATTGGCTGGTCAATGTGGTTTCTTGAGTATCTTTTCTGGAGAGAGTTGGG 558

Db 465 TACCGGTTATTGGTTGGTCAATGTGGTTTCTTGAATATCTTTTCTTGGAGAGAGTTGGG 524

QY 559 CCAAGGATGAAAGCACATTAAAGTCAGGCATCCAGCACTGAGTGATTTCCTCTTCCCT 618

Db 525 CCAAGGATGAAAGCACACATAAGTCAGGCCTACAGCAACTGAGGATTTCCTCCACTTCCCT 584

QY 619 TTTGGCTAGCTCTTGTGTAAGGAACGGGTTTACACAGGCCAAACTATTAGTGTCTC 678

Db 585 TTTGGTTGGCTCTATTGTTAGAGGAACCTGCTTTACACAGGCCAAACTATTAGTGTCTC 644

QY 679 AGGAATATGCCACTTCCACTGGATTGCTGTTCTCTAGAAATGTTTGA 726

Db 645 AGGAGTATGCAGCCTCAGCTGGATTGCCCTGTTCTCTAGAAATGTTTGA 692

RESULT 12

AW695931

LOCUS

DEFINITION

NF100G06ST1F1051 Developing stem Medicago truncatula cDNA clone NF100G06ST 5', mRNA sequence.

ACCESSION

AW695931

VERSION

AW695931.1 GI:7570693

KEYWORDS

EST.

SOURCE

Medicago truncatula (barrel medic)

ORGANISM

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

REFERENCE

1 (bases 1 to 656)

AUTHORS

He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon,R.A.

TITLE

Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula stem library

JOURNAL

Unpublished (2000)

COMMENT

Contact: Dixon RA



Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 221 7302  
Fax: 580 221 7380  
Email: radixon@noble.org  
Insert Length: 656 Std Error: 0.00  
Plate: 100 row: G column: 06  
Seq primer: TCACACAGGAAACAGCTATGAC.  
Location/Qualifiers

## FEATURES

source  
1..656  
/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/db\_xref="taxon:3880"  
/clone="NF100G06ST"  
/tissue\_type="stem"  
/dev\_stage="Pooled developmental"  
/clone\_lib="Developing stem"  
/note="Vector: Lambda Zap; Contains a mixture of  
internodal stem segments"

## ORIGIN

Query Match 30.8%; Score 461.2; DB 10; Length 656;  
Best Local Similarity 84.3%; Pred. No. 2e-69;  
Matches 531; Conservative 0; Mismatches 98; Indels 1; Gaps 1;

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QY 124 GCATGGCTANTGCAGCAGCGGCGGTGGGTACCATGGGCGCTGCTTCTTCGCTCCG 183
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 10 GTATGCCAATTTACCGGCAGCTGTGATCATCCATTGGGTATCTCTTCTTCGTTCTG 69

QY 184 GCCTCCTTGTTAATCTCATTCAGGCAATATGCTATGTCGTGTAAGCCGGTGTGAAAA 243
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 70 GTCTCATCGTTAATCATTCATTCAGGCAACATGCTTTGTGATTTTGAGACCTTTTCAAAGA 129

QY 244 GTTTGTACAGAGGATCAACCGGGTAGTAGCAGAGCTTGTGGCTGGAGCTTGTATGGC 303
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 130 ATTTGTACAGACGGATCAACAGAAATGTTGGCAGAACTTCTTTGGCTCGAGCTTGTGGA 189

QY 304 TTATTGATGGTGGGAGGAGTTAAGGTCCAAATATTCAGATCATGAAACCTTTCGTT 363
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 190 TTTTGTGATGGTGGGCTGTTGTCAGATCCAAATATTCAGATCCGAAACCTTTCGTT 249

QY 364 TAATGGTTAAAGAGCATGCACCTTGTGATAAGCAATACAGAACTGATATTGATGGCTTG 423
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 250 TCATGGGTACGGAGCATGCTCTTGTATATATCCAAATACAGAACTGATGATGGCTTG 309

QY 424 TTGGATGGTTTCAGCTCAGCGTTTCAGTTGTCTTGGCAGCACTCTAGCTGTGATGAAGA 483
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 310 TTGGATGGATTTTAGCTCAGCGTTTCAGGATGCCCTTGGTAGCACGCTTGTGATGAAGA 369

QY 484 AATCTTCAAAGTTTCTGCCGGTCAATGGCTGGTCAATGTGGTTTCTGAGTATCTTTTC 543
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 370 AATCATCTAAGTTTCTGCCGGTCAATGGGTGGTCAATGTGGTTTCTGATATCTTTCT 429

QY 544 TGGAGAGAAGTTGGGCCAAGGATGAAAGACATTAAGTCAGGCATCCAGCGACTGAGTG 603
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 430 TGGAGAGAATTTGGGCCAAGGATGAAAGACATTAAGTCAGGCATCCAGCAACTGCGGG 489

QY 604 ATTTCCCTCTCCCTTTTGGCTAGCTCTCTTTGTAGAAGGAACGGCTTTTACACAGGCCA 663
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 490 ATTTCCCTCTCCCTTTTGGCTAGCTCTCTTTGTAGAAGGAACCTGCTTTACACAGGCCA 549

QY 664 AACTATTAGCTGCTCAGGAATATGCCACTTCCACTTGCATTCCTGCTAGAAATGTTT 723
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Db 550 AATTATTAGCCGCTCAGGAATATGCAACCTCACTGGATTGCTGCTTCTAGAAACGTTT 609

QY 724 TGA-TTCCAAGAACTAAGGGTTTGTGTTCT 752
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Db 610 TGATTTCCAAGAACTAAGGGGGTTTGTGTTT 639
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## LOCUS

DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CD400176 466 bp mRNA linear EST 07-JUN-2003  
Gm ck21948 Soybean induced by Salicylic Acid Glycine max cDNA 3',  
mRNA sequence.  
CD400176  
CD400176.1 GI:31458148  
EST.  
Glycine max (soybean)  
Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.

## REFERENCE

## AUTHORS

1. (bases 1 to 466)

Tian, A.-G., Wang, J., Cui, P., Han, Y.-J., Xu, H., Cong, L.-J.,  
Huang, X.-G., Wang, X.-L., Jiao, Y.-Z., Wang, B.-J., Wang, Y.-J.,  
Zhang, J.-S., Chen, S.-Y. and Yu, J.

Soybean Expressed Sequence Tags Sequencing

Unpublished (2003)

Contact: Chen S-Y

Plant Biotechnology Laboratory

Institute of Genetics and Developmental Biology, CAS, China

Datun road, Beijing 100101, China

Tel: 86-10-64886859

Fax: 86-10-64873428

Email: sychen@genetics.ac.cn

Email: sychen@genetics.ac.cn

Seq primer: T7 primer.

Location/Qualifiers

1..466

## FEATURES

## source

/organism="Glycine max"

/mol\_type="mRNA"

/cultivar="Kefeng 1"

/db\_xref="taxon:3847"

/tissue\_type="Seedlings"

/dev\_stage="two-week seedlings"

/lab\_host="XLI-Blue MRF" strain"

/clone\_lib="Soybean induced by Salicylic Acid"

/note="Vector: pBluescript SK+; Site 1: EcoR I; Site 2:

Xho I; The cDNA library was constructed by He, C-y from

mRNA isolated from two-week seedlings (cultivar Kefeng 1)

treated by spraying 2.0mM salicylic acid for 24, 36, 48

and 72 h. Complementary DNA was synthesized from mRNA

using a primer consisting of a poly(dT) sequence with a

XhoI restriction site. EcoRI adapters were ligated to the

blunt-ended cDNA fragments followed by XhoI digestion. The

cDNA fragments were directionally cloned into the

EcoRI-XhoI restriction site of the pBluescript vector. The

ligated cDNA fragments were transformed into XLI-Blue MRF

host cells (Stratagene)."

## ORIGIN

Query Match 29.6%; Score 442.8; DB 14; Length 466;  
Best Local Similarity 99.3%; Pred. No. 3.3e-66;  
Matches 455; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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QY 1020 ACTGGTCGACCAATAAGTCTCTTCTGGTAGTTATATCTTGGCGGTCTGGTGTGCG 1079
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 458 ACTGGTCGACCAATAAGTCTCTTCTGGTAGTTATATCTTGGCGGTCTGGTGTGCG 399

QY 1080 GGGTCTGTAAAGTTCCTGCAATGGTCTCGTTACTCTCTTCTGGAAGGGTGTGCATTT 1139
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 398 GGGTCTGTAAAGTTCCTGCAATGGTCTCGTTACTCTCTTCTGGAAGGGTGTGCATTT 339

QY 1140 TCAGCTTTTGGTTTGGCAGTTGTTACTGCACTTATGCAAAATTCGATTCATTCACAG 1199
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 338 TCAGCTTTTGGTTTGGCAGTTGTTACTGCACTTATGCAAAATTCGATTCATTCACAG 279

QY 1200 TCAGAGCGTTCAACCCGGCCCAAGATCGTGCCTGCAAAAGTCAAAAACAGGGTCTTGA 1259
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 278 TCAGAGCGTTCAACCCGGCCCAAGATCGTGCCTGCAAAAGTCAAAAACAGGGTCTTGA 219

QY 1260 TTTATTGGCGGAACHTAAAGTTGCATTTATGTGATGAGTCACTGATCAATTAATCACTT 1319
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Db 218 TTTATTGGGAACTTAAAGTTGGATTATGTGTGATGAGTGACTCATGTAATACTCATT 159

QY 1320 ATTTTGCTTTCAACATCTTATCATAGTATGCTTCTTATTTCTATATATGTAAT 1379

Db 158 ATTTTGCTTTCAACATCTTATCATAGTATGCTTCTTATTTCTATATATGTAAT 99

QY 1380 GCTATCGATTTCATTTGTTTAAATTAATTAGGATATCCTTTTGTATTGACAGTCTAGGG 1439

Db 98 GCTATCGATTTCATTTGTTTAAATTAATTAGGATATCCTTTTGTATTGACAGTCTAGGG 39

QY 1440 GATGGC-CTAGAAAAATTCACACCTATTTTATTTTA 1476

Db 38 GATGGCACTAGAAAAATTCACACCTATTTTATTTTA 1

RESULT 14

LOCUS CB970126 670 bp mRNA linear EST 30-APR-2003

DEFINITION CAB10003\_I1a\_Fa\_D05 Cabernet Sauvignon Flower Pre-bloom - CAB1

CB970126 Vitis vinifera cDNA clone CAB10003\_I1a\_Fa\_D05 5', mRNA sequence.

ACCESSION CB970126.1 GI:30252575

VERSION EST.

KEYWORDS Vitis vinifera

SOURCE Vitis vinifera

ORGANISM Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 670)

AUTHORS Goes da Silva,F., Iandolino,A., Lim,H., Baek,J., Jones,K. and Cook,D.

TITLE Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon' berries at various developmental stages

JOURNAL Unpublished (2003)

COMMENT Contact: Douglas Cook, PhD

CAES Genome Facility

UC Davis, Plant Pathology

One Shields Ave, Davis, CA 95616, USA

Tel: 530 754 6561

Fax: 530 754 6617

Email: drcook@ucdavis.edu

Seq primer: ACGTACCGGACATATGCC.

FEATURES

source

1..670

Location/Qualifiers

/organism="Vitis vinifera"

/mol\_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db\_xref="taxon:29760"

/clone="CAB10003\_I1a\_Fa\_D05"

/sex="Hermaphrodite"

/dev\_stage="Pre-bloom"

/lab\_host="DH5alpha"

/clone\_lib="Cabernet Sauvignon Flower Pre-bloom - CAB1"

/note="Organ: Flower - Pre-bloom; Vector: pDNR; Site 1: Sfil; Site 2: Sfil; CAB1 is a cDNA library of Vitis vinifera cv. 'Cabernet Sauvignon' Clone 8 flowers. Samples were collected approximately eleven days before onset of bloom (clusters at this stage were fully developed and flowers with calyptras or caps still attached. Sampled vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows:

5'-AAGCAGTGGTATCAACGACAGTGGCCATTACGCCGGG-3' and

5'-ATTCTAGAGCGAGCGCGGCACATG-dT(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

ORIGIN

Query Match 29.1%; Score 436.4; DB 14; Length 670;

Best Local Similarity 81.2%; Pred. No. 3.5e-65;

Matches 506; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 122 GGGCATGGCTATTGCAGCAGCGGCGTGGTGGTACCATTTGGCCTGCTCTTCTTGGCCTC 181

Db 48 GGATATGGCGATTGCAGCGGCTGCCGTTGCCGTTGGTCTTCTTCTTCCACCTC 107

QY 182 CGGCTCTCTTGTAAATCTCATTCAGGCAATATGCTATGTCGTAAGCCGGTGTGAA 241

Db 108 CGGCTTGTAGTTAAATCTCATTCAGGCAATTTGTTTCATCCTTTAGGCCTCTGTCAA 167

QY 242 AAGTTTGTACAGAGGATCAACCCGGTAGTAGCAGAGCTCTTTGGGCTGGAGTTGTATG 301

Db 168 AAGTACATACAGAGGATCAACAGAGTGGTAGCAGAATTATTATGGCTCGAGCTTGTGTG 227

QY 302 GCTTATTGATTGGTGGCAGGAGTAAGTCCAAATATTCACAGATCATGAAACCTTTTCG 361

Db 228 GCTTATTGATTGGTGGCAGGAGTAAGTCCAACTGTACACAGATCCAGAAACGTTTCG 287

QY 362 TTTAATGGTAAAGAGCATGCACCTTGTGATAAGCAATCACAGAGTGTATTTGGCT 421

Db 288 CTTAATGGTAAAGAACATGCACCTTCTTATATCAACACACAGAGTGTATTTGGCT 347

QY 422 TGTTGGATGGGTTTCAGCTCAGCGTTCAGGTTGCTTGGCAGCACTCTAGCTGTGATGAA 481

Db 348 TGTTGGATGGGTTTGGCTCAGCGATCAGGTTGCTTGGCAGCACTCTAGCTGTGATGAA 407

QY 482 GAAATCTTCAAAGTTTCTGCCGTCATTTGGCTGGTCAATGTGGTTTCTTGAGTATCTTTT 541

Db 408 GAAATCATCAAATTCCTTCCGGTGATAGTTGCTCAATGTGGTTTCTTGAGTATTTATT 467

QY 542 TCTGAGAGAAAGTTGGGCCAAGGATGAAAGCACATTAAGTCAGGCATCCAGCGACTGAG 601

Db 468 TCTGAAAAGAACTGGGCCAAGGATGAAAGCAATAAAGTCAGGTCCTTCTACGATCAA 527

QY 602 TGATTTCCCTCTTCCCTTTTGGCTAGCTCTCTTTGTAGAAAGGACGCGTTTTCACAGGC 661

Db 528 GGACTACCTCAGCCTTTTGGTTGGCTCTTTTGTGAGGAACTCGCTTTTACAGAGGC 587

QY 662 CAAACTATTAGTCTCAGGAATATGCCACTTCCACTGGATTGCTGTTTCTAGAAATGT 721

Db 588 NAAGCTTTTAGAGCTCAAGAATATGCAACTGCATCGGGTTGCTGTTTCTAGAAATGT 647

QY 722 TTTGATTCCAAGAACTAAGGGTT 744

Db 648 TCTGATTTCCCGTACTAAGGGTT 670

RESULT 15

BQ403131

LOCUS BQ403131 685 bp mRNA linear EST 22-MAY-2002

DEFINITION GA\_Ed0054C03f Gossypium arboreum 7-10 dpa fiber library Gossypium

arboeum cDNA clone GA\_Ed0054C03f, mRNA sequence.

ACCESSION BQ403131

VERSION BQ403131.1 GI:21090818

KEYWORDS EST.

SOURCE Gossypium arboreum

ORGANISM Gossypium arboreum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.

REFERENCE 1 (bases 1 to 685)

AUTHORS Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.

TITLE An integrated analysis of the genetics, development, and evolution of the cotton fiber

JOURNAL Unpublished (2000)

COMMENT Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Total High Quality bases = 521

Seq primer: TAATACGACTCACTATAGG

High quality sequence start: 3  
High quality sequence stop: 637.  
FEATURES  
source  
1. .685  
/organism="Gossypium arboreum"  
/mol\_type="mRNA"  
/strain="AKA"  
/cultivar="8400"  
/db\_xref="taxon:29729"  
/clone="GA\_Ed0054C03f"  
/tissue\_type="Fibers isolated from bolls harvested 7-10 dpa"  
/lab\_host="E. coli"  
/clone\_lib="Gossypium arboreum 7-10 dpa fiber library"  
/note="Vector: pBK-CMV; Site\_1: EcoRI; Site\_2: XhoI"

ORIGIN

Query Match 29.0%; Score 434.4; DB 13; Length 685;  
Best Local Similarity 79.2%; Pred. No. 7.7e-65;  
Matches 513; Conservative 0; Mismatches 135; Indels 0; Gaps 0;  
QY 111 TGGGCTGGGCTGGGCATGGCTATTGCAGCAGCGGCCGTGGTGGTACCATTTGGGCCCTGCTC 170  
Db 38 TTGGCTGTTCTGTCCATGGCGATTGCAGCGGCAGCTGTATCGTCCCATTTGGGCCCTTCTT 97  
QY 171 TTCTTGGCTCCGGCCTCCTTGTAAATCTCATTTCAGGCAATATGCTATGTCGTTAAGG 230  
Db 98 TTCTTCATCTCCGGCCTCGCTGTGAATCTCATTTCAGGCGAGTATGCTTGTCTTATCGA 157  
QY 231 CCGGTGTCGAAAAGTTTGTACAGAAGGATCAACCGGCTAGTAGCAGAGCTCTTGTGGCTG 290  
Db 158 CCACTGTCCAAGAACACATATAGAAAGATCAATAGGGTATTGGCAGAGTTGTTGTGGCTG 217  
QY 291 GAGCTTGATGGCTTATTGATTGGTGGGCGAGGATTAGGTCCTCAAAATTCACAGATCAT 350  
Db 218 CAACCTGGTTGGCTGGTTGATTGGTGGGCGAGCGTTAAGATTGAAGTTTCGCAGATCAT 277  
QY 351 GAAACCTTTCCTTTAATGSGTAAAGAGCATGCACCTTGATAGATAAGCAATCACAGAAGTAT 410  
Db 278 GAAAGCTTCAATTTAATGSGTAAGGAACATGCCCTTGTCTATATGCAATCACAGAAGTAT 337  
QY 411 ATTGATTGGCTTGTGGATGGGTTTCAGCTCAGCGTTTCAGGTTGTCTGGCAGCACTCTA 470  
Db 338 ATTGATTGGTTAGTTGGATGGGTTTTCAGCAGAGGTCAGGTTGTCTGGCAGTACATTA 397  
QY 471 GCTGTGATGAAGAAATCTTCAAAAGTTTCCTCCGGTTCATTGGCTGGTCAATGTGGTTTCT 530  
Db 398 GCTGTAATGAAGAAATCATCAAAATTCCTCCGGTTCATAGGTTGGTCAATGTGGTTTCT 457  
QY 531 GAGTATCTTTTCTGGAGAGAAGTTGGGCAAGGATGAAAGCACATTAAGTCAGGCATC 590  
Db 458 GAGTATCTGTTTTTGAACCAAGCTGGGCCAAGGATGAAACACATTAAGGCGAGGTCCT 517  
QY 591 CAGCGACTGAGTGATTTCCTCTTCCCTTTTGGCTAGCTCTCTTTGAGAAGGAACCGGT 650  
Db 518 CAACGTTTTAAAGGACTTCCACCGGCCATTTTGGTTGGCACTTTTGTAGAAGGAACTCNG 577  
QY 651 TTTACACAGGCCAAACTATTAGCTGCTCAGGAATATGCCACTTCCACTGGATTGCCTGTT 710  
Db 578 TTTACACAAGCAAGCTTCTAGCAGCTCAAGAATATGCAACCTCACAGGATTGCCTGTA 637  
QY 711 CCTAGAAATGTTTGTATTCGAAGAACTAAGGGTTTGTGTTCTGCAGTA 758  
Db 638 CCTANAAATGTTNTAATTCCTCGTACAAAGGGTTTGTGTTTCANCCGTA 685

OM protein - protein search, using sw model

Run on: July 7, 2004, 13:36:58 ; Search time 45 Seconds  
(without alignments)  
2643.341 Million cell updates/sec

Title: US-09-914-098-56  
Perfect score: 1935  
Sequence: 1 MAIAAAVVVPLGLFFASG.....QSERNPAAKIVPAKSKNKGKGS 377

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL 25:\*
- 1: sp\_archaea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_mhc:\*
  - 8: sp\_organelle:\*
  - 9: sp\_phage:\*
  - 10: sp\_plant:\*
  - 11: sp\_rodent:\*
  - 12: sp\_virus:\*
  - 13: sp\_vertibrate:\*
  - 14: sp\_unclassified:\*
  - 15: sp\_rvirus:\*
  - 16: sp\_bacteriap:\*
  - 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1567	81.0	390	10 Q9XFW4	Q9xw4 brassica na
2	1564	80.8	389	10 Q8LG50	Q8lg50 arabidopsis
3	1519	78.5	377	10 Q40119	Q40119 limnanthes
4	1450.5	75.0	374	10 Q41745	Q41745 zea mays (m
5	1336	69.0	306	10 Q9SDN3	Q9sdn3 prunus dulc
6	1277	66.0	376	10 Q9SVX8	Q9svx8 arabidopsis
7	1161.5	60.0	310	10 Q9SYC8	Q9syc8 arabidopsis
8	1156.5	59.8	311	10 Q39317	Q39317 brassica na
9	844.5	43.6	237	10 Q7X9L2	Q7x9l2 triticum ae
10	606	31.3	376	11 Q9D517	Q9d517 m adult mal
11	599	31.0	376	11 Q7TT39	Q7tt39 mus musculu
12	595.5	30.8	376	13 Q7ZY11	Q7zyi1 xenopus lae
13	595	30.7	386	5 Q9VV51	Q9vv51 drosophila
14	587	30.3	377	13 Q7ZWC9	Q7zwc9 brachyphila
15	579	29.9	380	5 Q9VW49	Q9vw49 drosophila
16	551.5	28.5	378	11 Q8K4X7	Q8k4x7 m lysophosp

17	502.5	26.0	314	11 Q8BST2	Q8bst2 mus musculu
18	441	22.8	399	10 Q8LQR3	Q8lqr3 oryza sativ
19	415	21.4	378	10 Q8L4Y2	Q8l4y2 arabidopsis
20	414	21.4	373	10 Q9SSH0	Q9ssh0 arabidopsis
21	414	21.4	393	10 Q9C9P8	Q9c9p8 arabidopsis
22	400	20.7	375	10 Q9LHN4	Q9lhn4 arabidopsis
23	310.5	16.0	350	3 Q94361	Q94361 schizosacch
24	287	14.8	344	5 Q16526	Q16526 caenorhabdi
25	269	13.9	386	5 Q95R12	Q95r12 caenorhabdi
26	253.5	13.1	399	5 Q23087	Q23087 caenorhabdi
27	250	12.9	439	5 Q20800	Q20800 caenorhabdi
28	235.5	12.2	308	4 Q8N1Q7	Q8nlq7 homo sapien
29	202.5	10.5	281	5 Q8SS20	Q8ss20 encephalito
30	187	9.7	357	5 Q8SR20	Q8sr20 encephalito
31	180.5	9.3	370	11 Q91YX5	Q91yx5 mus musculu
32	176.5	9.1	404	13 Q72T38	Q7zt38 xenopus lae
33	173	8.9	300	16 Q83A38	Q83a38 coxiella bu
34	172	8.9	295	16 Q88R02	Q88r02 pseudomonas
35	168.5	8.7	299	16 Q88AE0	Q88ae0 pseudomonas
36	162	8.4	292	16 Q87KC2	Q87kc2 vibrio para
37	160.5	8.3	304	16 Q915A6	Q915a6 pseudomonas
38	148	7.6	310	16 Q8X8H2	Q8x8h2 escherichia
39	148	7.6	318	16 Q8FBH4	Q8fbh4 escherichia
40	145.5	7.5	296	16 Q83FB3	Q83fb3 coxiella bu
41	144	7.4	310	16 Q7UB62	Q7ub62 shigella fl
42	144	7.4	318	16 Q83IV6	Q83iv6 shigella fl
43	143	7.4	415	5 O01882	O01882 caenorhabdi
44	142.5	7.4	300	16 Q8XQC1	Q8xqc1 ralstonia s
45	135.5	7.0	428	5 Q95R03	Q95r03 caenorhabdi

ALIGNMENTS

RESULT 1

Q9XFW4 ID Q9XFW4 PRELIMINARY; PRT; 390 AA.  
AC Q9XFW4;  
DT 01-NOV-1999 (Tremblrel. 12, Created)  
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
DE Acyl-CoA:1-acylglycerol-3-phosphate acyltransferase  
DE (EC 2.3.1.51).  
GN LPAAT.  
OS Brassica napus (Rape).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Brassicales; Brassicaceae; Brassica.  
OX NCBI\_TaxID=3708;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Developing siliques;  
RA Graefin zu Muenster A.; Wolter F.P.; Frentzen M.;  
RT "A cDNA encoding a microsomal 1-acylglycerol-3-phosphate  
RT acyltransferase of Brassica napus L.";  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Z95637; CAB09138.1; -;  
DR GO; GO:0003841; F:1-acylglycerol-3-phosphate O-acyltransferas. . .; IEA.  
DR GO; GO:0008415; F:acyltransferase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR002123; Acyltransferase.  
DR InterPro; IPR001092; HLH\_basic.  
DR Pfam; PF01553; Acyltransferase; 1.  
DR SMART; SM00563; PISC; 1.  
DR PROSITE; PS00038; HLH\_1; 1.  
DR Acyltransferase; Transferase.  
SQ SEQUENCE 390 AA; 43771 MW; F1446E1B30009C37 CRC64;

Query Match 81.0%; Score 1567; DB 10; Length 390;  
Best Local Similarity 77.8%; Pred. No. 2.9e-131;  
Matches 288; Conservative 43; Mismatches 39; Indels 0; Gaps 0;

Qy	5	AAAVVPLGLLFFASGLLVNLQIAICVVVVRPVSKSLYRRINRVVAEELWLELVLDWM	64
Dd	4	AAAIVPLGILFFISGLVWNLLQAVCYVLVRPMSKNTYRKINRVVAETLWLDELVIWDWM	63
Qy	65	AGVKVQIETHETFRIMGKEHALVISNHRSDIDWLGVWSAQRSGLGSTLAMKKSSKF	124
Dd	64	AGVKIQVADDETFRMGKEHALVVCNHRSDIDWLGVWILAQRSGCLGSALAMKKSSKF	123
Qy	125	LPVIGSMWFSEYLFLERSWAKDESTLKSGIQRLSDFPLPFWIALFVEGTFTFOAKLLAA	184
Dd	124	LPVIGSMWFSEYLFLERNWAKDESTLOSGLQLRINDFPFPFWIALFVEGTFTFEAKLKA	183
Qy	185	QEYATSTGLPVPRNVLI.PRTKGFFSAVSVMRSFVPAYDYVTVAIPKSSPAPTMRLRFKG	244
Dd	184	QEYAASELPVPRNVLI.PRTKGFFSAVSNMRSFVPAYDYMTVAIPKTSPPPTMLRLFQG	243
Qy	245	PSVVHVHIKRHLMKELPDTD EAVAQCWRDIFVAKDALLDKHMAEGTFSDOELQDTGRPIK	304
Dd	244	PSVVHVHIKCHSMKDLPEDPEDEIAQCWRDQFVAKDALLDKHIAADTFPGQEQNIGRP	303
Qy	305	SLLVVISWACLWAGSVKFLQWSSLSSWKGVAFSAFGLAVVTALMQILIQFSQSERSNP	364
Dd	304	SLAVVVSWACLLTLGAMKFLHWSNLFSSWKGIASFGLGIITLCMQIILRSSQSERSTP	363
Qy	365	AKIVPAKSKN	374
Dd	364	AKVAPAKPKO	373

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RESULT 2
Q8LGS0 PRELIMINARY; PRT; 389 AA.
AC Q8LGS0;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE 1-acylcerol-3-phosphate acyltransferase-like protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana.";
RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY084461; AAM61033.1; -.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002123; Acyltransferase.
DR InterPro; IPR001092; HLH basic.
DR Pfam; PF01553; Acyltransferase; 1.
DR SMART; SM00563; PISC; 1.
DR PROSITE; PS00038; HLH 1; 1.
KW Transferase; Acyltransferase.
SQ SEQUENCE 389 AA; 43706 MW; F34F73B2E2AC6837 CRC64;

```

Db	2	VIAAAVIVPLGLLFFISGLAVNLFOQAVCYVLRPLSKNTYRKINRVVAETLWLELVWIVD	61
QY	63	WWAGVKVQVIFTDHTFRLMGKEHALVISNHRSDIDWLGVGVSQAORSGCLGSTLAVMKSS	122
Db	62	WWAGVKIQVFNADNFTNRMGKEHALVVCNHRSDIDWLGVWILAORSGCLGSALAVMKSS	121
QY	123	KFLPVGWSMWFSEYLFLEERSWAKDESTLKSGLQRLSDFLPFWLALFVEGTRFTQAKLL	182
Db	122	KFLPVGWSMWFSEYLFLEERNWAKDESTLKSGLQRLSDFFRPFWLALFVEGTRFTEALK	181
QY	183	AAQEVATSTGLPVRNVLIPTKGFVSVAVSHMRSFVPAIYDVTVAI PKSSPAPTMLRLFK	242
Db	182	AAQEVAAASSELPIPRNVLIPTKSFVSVAVSNMRSFVPAIYDMVTVTIPKSPPTMLRLFK	241
QY	243	GQPSVVHVHIKRLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQDELQDTGRP	302
Db	242	GQPSVVHVHIKCHSKMDLPESDDAIAQWCRDOFVAKDALLDKHIAADTFPGQEQNIGRP	301
QY	303	IKSLVLVISWACLVVAGSVKFLOWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSERS	362
Db	302	IKSLAVVLSWACVLTGLGAKPLHWAQLFSSWKGITISALGLGIITLCMQILIRSSQSERS	361
QY	363	NPAKIVPAKSKN	374
Db	362	TPAKVVPAPKD	373

RESULT 3

Q40119 PRELIMINARY; PRT; 377 AA.

AC Q40119;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE 1-acyl-sn-glycerol-3-phosphate acyltransferase (Putative).

OS Limnathes douglasii (Douglas's meadowfoam).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Brassicales; Limnathaceae; Limnathes.

OX NCBI\_TaxID=28973;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96046746; PubMed=7579178;

RA Brown A.P., Brough C.L., Kroon J., Slabas A.R.;

RT "Identification of a cDNA that encodes a 1-acyl-sn-glycerol-3-phosphate acyltransferase from Limnathes douglasii.";

RL Plant Mol. Biol. 29:267-278(1995).

DR EMBL; Z48730; CAA88620.1; --

DR PIR; S60478; S60478.

DR GO; GO:0008415; F:acyltransferase activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR002123; Acyltransferase.

DR InterPro; IPR001092; HLH basic.

DR Pfam; PF01553; Acyltransferase; 1.

DR SMART; SM00563; PlsC; 1.

DR PROSITE; PS00038; HLH\_1; 1.

KW Acyltransferase; Transferase.

SQ SEQUENCE 377 AA; 442780 MW; 0DECDEF25D39687C CRC64;

3 IAAAVVPLGLLFFASGLLVNLIQAICYVVRPVSksLYRRINRVVAELLWLELVWLID 62 QY

Db 121 SSKFLPVIGSMWFSEYLFERNWAXDENTLKSGLQRLNDFPKPFWLALFVEGTRFTKAK 180
181 LLAQAEYATSTGLPVPRNVLIPTKGFVS AVSHMRSFVPAIYDVTVAIPKSSPAPTMRL 240
181 LLAQAEYAAAGLPVPRNVLIPTKGFVS AVSNMRSFVPAIYDLTVAIPKTTTEQPTMLRL 240
241 FKGQPSVVHVHIKRLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDOELQDTG 300
241 FRGKSSVVHVHLKRLMKDLPKTDGVAQWCKDQFISKDALLDKHVAEDTFSGLEVDIG 300
301 RPIKSLVVISWACL VVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE 360
301 RPMKSLVVVSWMCLCLGLVKFLQWSALLSSWKGMWTTFVLGIVTVLMMHILIRSSQSE 360
361 RSNPAK 366
361 HSTPAK 366
RESULT 4
Q41745
ID Q41745 PRELIMINARY; PRT; 374 AA.
AC Q41745;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE 1-acyl-glycerol-3-phosphate acyltransferase (Putative).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI\_TaxID=4577;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Black Mexican Sweet; TISSUE=Endosperm;
RX MEDLINE=95035993; PubMed=7948871;
RA Brown A.P., Coleman J., Tomney A.M., Watson M.D., Slabas A.R.;
RT "Isolation and characterization of a maize cDNA that complements a 1-
RT acyl sn-glycerol-3-phosphate acyltransferase mutant of E.coli and
RT encodes a protein which has similarities to other acyltransferases.";
RL Plant Mol. Biol. 26:211-223(1994).
DR EMBL; Z29518; CAA82638.1; -.
DR PIR; S52645; S52645.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002123; Acyltransferase.
DR InterPro; IPR001092; HLH basic.
DR Pfam; PF01553; Acyltransferase; 1.
DR SMART; SM00563; PlsC; 1.
DR PROSITE; PS00038; HLH\_1; 1.
KW Acyltransferase; Transferase.
SQ SEQUENCE 374 AA; 42571 MW; F1F5492CAFF24F93 CRC64;
Query Match 75.0%; Score 1450.5; DB 10; Length 374;
Best Local Similarity 70.7%; Pred. No. 6.8e-121;
Matches 265; Conservative 51; Mismatches 58; Indels 1; Gaps 1;
QY 1 MAIAAAVVPVPLGLLFFASGLLVNLIQAICYVVRPVSKSLYRRINRVVAELLWLLELWVL 60
Db 1 MAIPLVLVPLGLLFLSLGLIVNAIQAVLFTIRPFKSFYRRINRFLAELLWLQLVWV 60
QY 61 IDWWAGVKVQIFTDHEFRLMGKEHALVISNHRSDIDLWVGWVS AQRSGLGSTLAWMKK 120
Db 61 VDWAGVKVQLHADEETVRSMGKEHALIISNHRSDIDLWIGWILAQRSGLGSTLAWMKK 120
QY 121 SSKFLPVIGSMWFSEYLFERNWAXDENTLKSGLQRLNDFPKPFWLALFVEGTRFTQAK 180
Db 121 SSKFLPVIGSMWFSEYLFERNWAXDENTLKSGLQRLNDFPKPFWLALFVEGTRFTPAK 180
QY 181 LLAQAEYATSTGLPVPRNVLIPTKGFVS AVSHMRSFVPAIYDVTVAIPKSSPAPTMRL 240

Db 181 LLAQAEYAAAGLPAPRNVLIPTKGFVS AVSIMRDFVPAIYDVTTVIPKDSPOPTMLRI 240
QY 241 FKGQPSVVHVHIKRLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDOELQDTG 300
Db 241 LKGQSSVTVHRMKRHSMPKSDSDVSKWCKDIFVAKDALLDKHLATGTF-DEEIRPIG 299
QY 301 RPIKSLVVISWACL VVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE 360
Db 300 RPVKSLVTLFWSCLLLFGAIEFFKWTQLLSTWRGVAF TAAGMALVTGVMHVFIMFSQAE 359
QY 361 RSNPAKIVPAKSNK 375
Db 360 RSSSARAARNRVKKE 374
RESULT 5
Q9SDN3
ID Q9SDN3 PRELIMINARY; PRT; 306 AA.
AC Q9SDN3;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE 1-acyl-sn-glycerol-3-phosphate acyltransferase.
OS Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI\_TaxID=3755;
RN [1]
SEQUENCE FROM N.A.
RA Campalans A., Pages M., Messegue R.;
RT "Identification of differentially expressed genes during dehydration
RT in almond (Prunus amygdalus) using the cDNA-AFLP technique.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF213937; AAF20003.1; -.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002123; Acyltransferase.
DR InterPro; IPR001092; HLH basic.
DR Pfam; PF01553; Acyltransferase; 1.
DR SMART; SM00563; PlsC; 1.
DR PROSITE; PS00038; HLH\_1; 1.
KW Acyltransferase; Transferase.
SQ SEQUENCE 306 AA; 33993 MW; CBD334496E25908D CRC64;
Query Match 69.0%; Score 1336; DB 10; Length 306;
Best Local Similarity 84.5%; Pred. No. 8.5e-111;
Matches 250; Conservative 23; Mismatches 23; Indels 0; Gaps 0;
QY 81 MGKEHALVISNHRSDIDLWVGWVS AQRSGLGSTLAVMKSSKFLPVIGSMWFSEYLF 140
Db 1 MGKEHALVISNHRSDIDLWVGWVLAQRSGLGSSSLAVMKSSKFLPVIGSMWFSEYLF 60
QY 141 ERSWAKDESTLKSIGIQLSDPFLPFWLALFVEGTRFTQAKLLAAQEYATSTGLPVPRNV 200
Db 61 ERSWAKDEGTLKSGVQRLKDFPQPFWLALEFVEGTRFTQAKLLAAQEYAAATGLPVPRNV 120
QY 201 IPRTKGFVS AVSHMRSFVPAIYDVTVAIPKSSPAPTMRLPKGPSVTVHVKRHLMKEL 260
Db 121 IPRTKGFVTAVSQMRSFAPAIYDVTVAIPKSSPAPTMRLPEGRPSVTVHVKRHMVDL 180
QY 261 PDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDOELQDTGRPIKSLVVISWACL VVAGS 320
Db 181 PETDEAVAQWCKDIFVAKDALLDKHTVEQTFGQQQLKVTGRPLKSLVVITAWACLLILGA 240
QY 321 VKFLOWSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSERSNPAKIVPAKSNKG 376
Db 241 LKELYWSSLLSSWKGI AFSA LGVTVLMLQILIRFSQSERSTPAPVPTNNKNG 296
RESULT 6
Q9SYC8

ID Q9SYC8 PRELIMINARY; PRT; 376 AA.  
AC Q9SYC8;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Putative acyl-CoA:1-acylglycerol-3-phosphate acyltransferase.  
GN F11M15.12.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,  
RA Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,  
RA Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,  
RA Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,  
RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC006085; AAD30638.1; -.  
DR PIR; D96550;  
DR GO; GO:0008415; F:acyltransferase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR002123; Acyltransferase.  
DR InterPro; IPR001092; HLH basic.  
DR Pfam; PF01553; Acyltransferase.  
DR SMART; SM00563; Plsc; 1.  
DR PROSITE; PS00038; HLH\_1; 1.  
DR Acyltransferase; Transferase.  
KW Acyltransferase; Transferase.  
SQ SEQUENCE 376 AA; 43435 MW; 0B9AE143B09ED4D0 CRC64;

Query Match 66.0%; Score 1277; DB 10; Length 376;  
Best Local Similarity 62.3%; Pred. No. 2e-105;  
Matches 228; Conservative 62; Mismatches 76; Indels 0; Gaps 0;

QY 1 MAIAAAVVVPLGLLFFASGLLVNLIQAICYVVVVRPVSKSLYRINRVVAELWLELVL 60  
Db 1 MKIPALVFIPVGVLFISGLIVNIQLVFFIIVRPFSSRLYRINKNVAELWQLIWL 60  
QY 61 IDWAGVKVQIFTDHETFRMLMGKEHALVISNHRSDIDWLGVWSAQRSGCLGSLAVMKK 120  
Db 61 FDWWACIKINLYVDAETLELIGKEHALVLSNHRSDIDWLIGWYMAQRVGCGLSLAIMKK 120  
QY 121 SSKFLPVIGWSMWFSEYLFLEERSWAKDESTLKSGLQRLSDFFLPFWLALFVEGTRFTQAK 180  
Db 121 EAKYLPFIIGWSMWFSDYIFLEERSWAKDESTLKSGLQRLSDFFLPFWLALFVEGTRFTQAK 180  
QY 181 LLAQEYATSTGLPVRNVLIPTKGFVSASVSHMRSFVPAIYDVTVVAIPKSSPAPTMLRL 240  
Db 181 LEAQEYASIRSLPSRNVLIPTKGFVSASVSEIRSFVPAIYDVTVVHNQPTPTLLRM 240  
QY 241 FKQSVVHVHIKRLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQDELQDTG 300  
Db 241 FSGQSSEINLQMRHKKSELPEITDGGIAQWQDLFIITKDAQLEKFTKDVFSDELVEHQIN 300  
QY 301 RPIKSLLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAGLAVVTALMQILIQFSQSE 360  
Db 301 RPIKSLLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAGLAVVTALMQILIQFSQSE 360  
QY 361 RSNPAK 366  
Db 361 RSTPAK 366

RESULT 7  
Q9SVX9  
ID Q9SVX9 PRELIMINARY; PRT; 310 AA.  
AC Q9SVX9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE 1-acylcerol-3-phosphate acyltransferase-like protein.  
GN F15B8.160.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Benes V., Rechmann S., Borkova D., Ansoorge W., Mewes H.W.,  
RA Mayer K.F.X., Lemcke K., Schueller C., Quetier F., Salancoubat M.;  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL049660; CAB41190.1; -.  
DR PIR; T06755; T06755.  
DR GO; GO:0008415; F:acyltransferase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR002123; Acyltransferase.  
DR InterPro; IPR001092; HLH basic.  
DR Pfam; PF01553; Acyltransferase; 1.  
DR SMART; SM00563; Plsc; 1.  
DR PROSITE; PS00038; HLH\_1; 1.  
KW Acyltransferase; Transferase.  
SQ SEQUENCE 310 AA; 34382 MW; A1B5748F37B625AD CRC64;

Query Match 60.0%; Score 1161.5; DB 10; Length 310;  
Best Local Similarity 61.3%; Pred. No. 3.1e-95;  
Matches 228; Conservative 30; Mismatches 35; Indels 79; Gaps 1;

QY 3 IAATAVVVPLGLLFFASGLLVNLIQAICYVVVVRPVSKSLYRINRVVAELWLELVL 62  
Db 2 VIAAAVIVPLGLLFFISGLAVNLF-----QKSGCLGSALAVMKSS 42  
QY 63 WWAGVKVQIFTDHETFRMLMGKEHALVISNHRSDIDWLGVWSAQRSGCLGSLAVMKSS 122  
Db 26 -----QKSGCLGSALAVMKSS 42  
QY 123 KFLPVIGWSMWFSEYLFLEERSWAKDESTLKSGLQRLSDFFLPFWLALFVEGTRFTQAKLL 182  
Db 43 KFLPVIGWSMWFSEYLFLEERSWAKDESTLKSGLQRLSDFFLPFWLALFVEGTRFTQAKLK 102  
QY 183 AAQEYATSTGLPVRNVLIPTKGFVSASVSHMRSFVPAIYDVTVVAIPKSSPAPTMLRLFK 242  
Db 103 AAQEYAAASSELPIPRNVLIPTKGFVSASVSHMRSFVPAIYDVTVVTPKTSPPPTMLRLFK 162  
QY 243 GQPSVVHVHIKRLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQDELQDTGRP 302  
Db 163 GQPSVVHVHIKCHSMKDLPESDATAQWCRDQFVAKDALLDKHIAADTFPGQEQNIGRP 222  
QY 303 IKSLLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAGLAVVTALMQILIQFSQSERS 362  
Db 223 IKSLAVVLSWACVLTGLAIFLHWAQLFSSWKGITISALGLGITLQCMQILIRSSQSERS 282  
QY 363 NPAKIVPAKSKN 374  
Db 283 TPAKVVPAPKPKD 294

RESULT 8  
Q93317  
ID Q93317 PRELIMINARY; PRT; 311 AA.  
AC Q93317;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE 1-acyl-sn-glycerol-3-phosphate acyltransferase.  
OS Brassica napus (Rape).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;



OC eurosids II; Brassicales; Brassicaceae; Brassica.  
OX NCBI\_TaxID=3708;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. jet neuf;  
RA Brown A.P., Brough C.L., Kroon J.T., Slabas A.R.;  
RT "Nucleotide sequence of a cDNA for a putative 1-acyl sn-glycerol-3-  
RT phosphate acyltransferase from rape.";  
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Z49860; CAA90019.1; -.  
DR PIR; T07936; T07936.  
DR GO; GO:0008415; F:acyltransferase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR002123; Acyltransferase.  
DR InterPro; IPR001092; HLH basic.  
DR Pfam; PF01553; Acyltransferase; 1.  
DR SMART; SM00563; PlsC; 1.  
DR PROSITE; PS00038; HLH\_1; 1.  
KW Acyltransferase; Transferase.  
SQ SEQUENCE 311 AA; 34446 MW; C80FFEF97A144FBB CRC64;  
  
Query Match 59.8%; Score 1156.5; DB 10; Length 311;  
Best Local Similarity 61.4%; Pred. No. 8.8e-95;  
Matches 227; Conservative 33; Mismatches 31; Indels 79; Gaps 1;  
  
QY 5 AAAVVVPLGLLFFASGLLVNLIQAICYVVVVRPVSKSLYRRINRVVAELLWLELVLDWM 64  
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 25  
4 AAAVIVPLGILFFISGLVNVLL-----  
  
QY 65 AGVKVQIFTDHTETFRMLGKEHALVISNHRSDIDLWVGWVSQRSGLGSLTAVMKKSKF 124  
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 44  
26 -----ORSGCLGSALAVMKKSKF  
  
QY 125 LPVIGWSMWFSEYLFLEERSWAKDESTLKSGLQRLSDPPLPFWLALFVEGTRFTQAKLLAA 184  
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 104  
45 LPVIGWSMWFSEYLFLEERNWAKDESTLKSGLQRLNDPFRPFWLALFVEGTRFTEAKLAA  
  
QY 185 QEYATSTGLPVRNVLIPRTKGFVSASVSHMRSFVPAIYDVTVAIPKSSAPTMLRLFKGQ 244  
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 164  
105 QEYAAASSELPPVRNVLIPRTKGFVSASVSNMRSFVPAIYDVTVAIPKTSPPPTMLRLFKGQ  
  
QY 245 PSVVHVHIKRLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQDELQDTGRPIK 304  
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 224  
165 PSVVHVHIKCHSMKDLPESEDEIAQWCRDQFVTKDALLDXHIAADTFAGQKEQNIGRPIK  
  
QY 305 SLLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQIILQFSQSERSNP 364  
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 284  
225 SLAVVLSWACLTLTGAMKFLHWSNLFSSWKGLSALGIGITLCMQIILRSSQSERSSTP  
  
QY 365 AKIVPAKSKN 374  
Db |||:|||||: 294  
285 AKVAPAKPKD  
  
RESULT 9  
Q7X9L2  
ID Q7X9L2 PRELIMINARY; PRT; 237 AA.  
AC Q7X9L2;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE 1-acyl-glycerol-3-phosphate acyltransferase (Fragment).  
OS Triticum aestivum (Wheat).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Triticum.  
OX NCBI\_TaxID=4565;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. PH 82-2-2; TISSUE=Seed;  
RA Li J.R., Wang F., Li Q.Z., Zhang X.S.;  
RT "Gene isolation and expression of 1-acyl-glycerol-3-phosphate

RT acyltransferase.";  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF479037; AAP80656.1; -.  
KW Acyltransferase; Transferase.  
FT NCN TER 1  
SQ SEQUENCE 237 AA; 26693 MW; F4A164BDA47243A1 CRC64;  
  
Query Match 43.6%; Score 844.5; DB 10; Length 237;  
Best Local Similarity 74.3%; Pred. No. 4.1e-67;  
Matches 162; Conservative 20; Mismatches 35; Indels 1; Gaps 1;  
  
QY 86 ALVISNHRSDIDLWVGWVSQRSGLGSLTAVMKKSKFPLVIGWSMWFSEYLFLEERSWA 145  
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 62  
3 ALLISNHRSDIDLWVGWILAQSRSGCLGSAIAIMKKSKFPLVIGWSMWFSEYLFLEERSWA  
  
QY 146 KDESTLKSGLQRLSDPPLPFWLALFVEGTRFTQAKLLAAQFYATSTGLPVRNVLIPRTK 205  
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 122  
63 KDEKTLKSGLQRLKDFPRSFWLALFVEGTRFTPAKLLAAQFYAISQGLTAPRNVLIPTK  
  
QY 206 GFVSASVSHMRSFVPAIYDVTVAIPKSSPAPTMLRLFKGQSVVHVHIKRLMKELPDTDE 265  
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 182  
123 GFVSASVIMRDFVPAIYDVTIIPEDSPKPTMLRLQGSVVHVRIKRHSMDMPNSDE  
  
QY 266 AVAQWCRDIFVAKDALLDKHMAEGTFSQDELQDTGRPI 303  
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 219  
183 DVSKWCKDIFVAXDALLGQTYSNWSF-DXENIPIXRPM  
  
RESULT 10  
Q9D517  
ID Q9D517 PRELIMINARY; PRT; 376 AA.  
AC Q9D517;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Adult male testis cDNA, RIKEN full-length enriched library,  
DE clone:4930526L14 product:1-acylglycerol-3-phosphate O-acyltransferase  
DE 3, full insert sequence (1-acylglycerol-3-phosphate-gamma)  
DE (EC 2.3.1.51) (1-acylglycerol-3-phosphate O-acyltransferase 3).  
GN AGPAT3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,  
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,  
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,  
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,  
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
RA Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Head, Liver, and Testis;  
RC MEDLINE=22354683; PubMed=12466851;  
RX The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RA "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573 (2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX MEDLINE=21085660; PubMed=11217851;  
RA RIKEN FANTOM Consortium;

RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:695-690(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX Lu B., Jiang Y.J., Chan M., Choy P.C.;
RT "Identification and characterization of 1-acylglycerol-3-phosphate
acyltransferase-gamma.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK015906; BAB30025.2; -
DR EMBL; AY167588; AAN75574.1; -
DR EMBL; AK075715; BAC35905.1; -
DR EMBL; AK076414; BAC36329.1; -
DR MGD; MGI:1336186; Agpat3.
DR GO; GO:0003841; F:1-acylglycerol-3-phosphate O-acyltransferase. . .; IEA.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002123; Acyltransferase.
DR Pfam; PF01553; Acyltransferase; 1.
DR SMART; SM00563; PlcC; 1.
DR Acyltransferase; Transferase.
SQ SEQUENCE 376 AA; 43296 MW; 6F8C8970404B2EC1 CRC64;

Query Match 31.3%; Score 606; DB 11; Length 376;
Best Local Similarity 37.0%; Pred. No. 1.4e-45;
Matches 125; Conservative 72; Mismatches 129; Indels 12; Gaps 4;

QY 12 LGLLFFASGLLVNLIQAICYVVRPVSKSLYRRINRVVAELLMLELVLDWAGVKVQI 71
Db 17 IGFVVFVSGLIINFQ-LCTLALWPISKLYRRINCRLAYSLWSQLVLMLEWWSCTECL 75
QY 72 FTDHETFRMLMGKEHALVISNHRSDIDLWVGWVSQAQRSGCLGSLAVMKSSKFLPVIGWS 131
Db 76 FTDQATVDHFHKGHEVWVILNHNFEIDFLCGWTMCERFGLVSGSKVLAKRELLCVPLIGWT 135
QY 132 MWFSEYFLERSWAKDESTLKSQIRLSDFPLFWLALFVEGTRFTQAKLLAAQYATST 191
Db 136 WYFLEIVFCRKEEDRDTVIEGLRLADYPEYMWFLLYCEGTRFTETKTRISMEVAASK 195
QY 192 GLPVRNVLIPRTKGFVSANVSMRFSVPAIYDVTVAIPKSSAPTMLRLFKGQPSVVH 251
Db 196

[illegible]

RESULT 12  
Q7ZYI1  
ID Q7ZYI1  
PRELIMINARY; PRT; 376 AA.

01-JUN-2003 (TReMBLrel. 24, Created)  
 01-JUN-2003 (TReMBLrel. 24, Last sequence update)  
 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
 Similar to 1-acylglycerol-3-phosphate O-acyltransferase 3.  
*Xenopus laevis* (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI TaxID=8355;

RN [1]  
RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;  
PA Klein S., Strausberg R.;

RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC043776; AAH43776.1; -.

DR GO; GO:0008415; F:acyltransferase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR002123; Acyltransferase.

DR Pfam; PF01553; Acyltransferase; 1.  
DR SMART; SM00563; PLSC; 1.

KW	Transferase; Acyltransferase.
SEQUENCE	376 AA; 43685 MW; 62ADFDCBBBBB460D CRC64;

Query Match	Score	DB	Length
5	30.8	595.5	13
6	30.8	595.5	13
7	30.8	595.5	13
8	30.8	595.5	13
9	30.8	595.5	13
10	30.8	595.5	13
11	30.8	595.5	13
12	30.8	595.5	13
13	30.8	595.5	13
14	30.8	595.5	13
15	30.8	595.5	13
16	30.8	595.5	13
17	30.8	595.5	13
18	30.8	595.5	13
19	30.8	595.5	13
20	30.8	595.5	13
21	30.8	595.5	13
22	30.8	595.5	13
23	30.8	595.5	13
24	30.8	595.5	13
25	30.8	595.5	13
26	30.8	595.5	13
27	30.8	595.5	13
28	30.8	595.5	13
29	30.8	595.5	13
30	30.8	595.5	13
31	30.8	595.5	13
32	30.8	595.5	13
33	30.8	595.5	13
34	30.8	595.5	13
35	30.8	595.5	13
36	30.8	595.5	13
37	30.8	595.5	13
38	30.8	595.5	13
39	30.8	595.5	13
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41	30.8	595.5	13
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44	30.8	595.5	13
45	30.8	595.5	13
46	30.8	595.5	13
47	30.8	595.5	13
48	30.8	595.5	13
49	30.8	595.5	13
50	30.8	595.5	13
51	30.8	595.5	13
52	30.8	595.5	13
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54	30.8	595.5	13
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61	30.8	595.5	13
62	30.8	595.5	13
63	30.8	595.5	13
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65	30.8	595.5	13
66	30.8	595.5	13
67	30.8	595.5	13
68	30.8	595.5	13
69	30.8	595.5	13
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72	30.8	595.5	13
73	30.8	595.5	13
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77	30.8	595.5	13
78	30.8	595.5	13
79	30.8	595.5	13
80	30.8	595.5	13
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84	30.8	595.5	13
85	30.8	595.5	13
86	30.8	595.5	13
87	30.8	595.5	13
88	30.8	595.5	13
89	30.8	595.5	13
90	30.8	595.5	13
91	30.8	595.5	13
92	30.8	595.5	13
93	30.8	595.5	13
94	30.8	595.5	13
95	30.8	595.5	13
96	30.8	595.5	13

Best Local Similarity 34.4%; Pred. NO. 1.2e-44;  
Matches 118; Conservative 79; Mismatches 125; Indels 21; Gaps 5

QY 12 LGLLFFASGLLVNLIQAICYVVVVRPVSKSLYRINRVVAELLNLELVNLIIDWAGVKVQI 71

17 IGEFVVSGLIIINFIQ-LCTLPWGINKPLYRRINCRMAIYLLWSQLVMLEFWWSGTQCTL 75

QY 72 FTDHETRLMGKEHALVISNHRSDIDLWVGWVSAQRSGCLGSTLAVMKSSKFLPVIGWS 131

Db 76 FSDQKIDHFGKEHVIIILNHNVEIDFLCGWTMCERYVLGGSKVLAKELLMVPLIGWT 135

Qy 132 MWFSEVILFLERSWAKDESTLXSGIQRLSDFPIPFWALFVEGTRFTQAKLLAAQEYATST 191

Db 136 WYFLEIVFCRKWEEDRDVTIOGLKDLRDYPEYMWFLYCEGTRFTETKHKSMEVADKK 195

Qy 192 GLPVPRNVLI PRTKGFSVAVSHMESFVPAIYDVTVAIPKSSPAPMTLRIFKGQPSVVHH 251

Db 196 GLARLKHLLPRTGRGTTAVQCLRGTVSAVYDVTLSF-RGNKNPSLLGLIYKGYEADMC 254

QY 252 IKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDELQDTGRIKSLVVIS 311

Db 255 VRRFPLEEIPEDKEAAAWLHKLYQEKDALQEQYIQEGTFPTQIVPPRRP----- 305

Qy 312 WACLVTAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILI 354

Db 306 WTLL-----NFLFWATLLS-----PLFSFAIGIFASGSPLLI 338

RESULT 13  
Q9VW51

ID	Q9VV51	PRELIMINARY;	PRT;	386 AA.
AC	Q9VV51;	Q9VV50;		

DT 01-MAY-2000 (TRENBLrel. 13, Created)

01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
CG4729 protein (RE10780p).  
CG4729.  
Drosophila melanogaster (Fruit fly).  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
NCBI\_TaxID=7227;  
[1]  
SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).  
RC STRAIN=Berkeley;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffe  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Bald  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Cha  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.  
RA Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleisc  
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ket  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Rees  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen T  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zh  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu S.  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*."  
RL Science 287:2185-2195(2000).  
RN [2]  
RC SEQUENCE FROM N.A.  
RC STRAIN=y;  
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Fris  
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Lia  
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Pa  
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin  
RA Celniker S.;  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Long;  
CC IsoId=Q9VVV51-1; Sequence=Displayed;  
CC Name=Short;  
CC IsoId=Q9VVV51-2; Sequence=VSP\_050280;  
DR EMBL; AE003527; AAF49471.1; -;  
DR EMBL; AE003527; AAF49472.1; -;  
DR EMBL; BT001546; AAN71301.1; -;  
DR FlyBase; FBgn0036623; CG4729.  
DR GO; GO:0008415; F-acyltransferase activity; IEA.  
DR GO; GO:0008152; P-metabolism; IEA.





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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.  
OM protein - protein search, using sw model  
Run on: July 7, 2004, 13:33:37 ; Search time 18 Seconds  
(without alignments)  
1090.580 Million cell updates/sec  
Title: US-09-914-098-56  
Perfect score: 1935  
Sequence: 1 MAIAAAVVVPLGLLEFASG.....QSERSNPAKIVPAKSKNKGK 377

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 141681 seqs, 52070155 residues  
Total number of hits satisfying chosen parameters: 141681  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					% Query Match		Description	
Result No.	Score	Match	Length	ID				
1	628	32.5	376	1 PLCC_HUMAN			Q9nrz7 homo sapien	
2	554.5	28.7	378	1 PLCD_HUMAN			Q9nrz5 homo sapien	
3	551.5	28.5	378	1 PLCD_RAT			Q924s1 rattus norv	
4	304	15.7	364	1 PLCE_HUMAN			Q9nuq2 homo sapien	
5	303	15.7	365	1 PLCE_MOUSE			Q9dle8 mus musculu	
6	271	14.0	397	1 YBP2_YEAST			P38226 saccharomyc	
7	247	12.8	396	1 YD18_YEAST			Q12185 saccharomyc	
8	186.5	9.6	370	1 Y205_HUMAN			Q92604 homo sapien	
9	148	7.6	310	1 YIHG_ECOLI			P32129 escherichia	
10	124.5	6.4	391	1 YT73_CAEEL			Q11087 caenorhabdi	
11	121	6.3	303	1 PLSC_YEAST			P33333 saccharomyc	
12	120	6.2	245	1 PLSC_ECOLI			P25647 escherichia	
13	120	6.2	245	1 PLSC_SALTY			P26974 salmonella	
14	118.5	6.1	281	1 PLSC_LIMAL			Q42868 limnanthes	
15	118.5	6.1	281	1 PLSC_LIMDO			Q42870 limnanthes	
16	115.5	6.0	240	1 PLSC_HAEIN			P44848 haemophilus	
17	109	5.6	278	1 PLCB_HUMAN			Q15120 homo sapien	
18	105	5.4	282	1 PLC2_CAEEL			Q23267 caenorhabdi	
19	100.5	5.2	722	1 GREX_CHLPN			Q92794 chlamydia p	
20	100	5.2	391	1 PER_DROIN			P91613 drosophila	
21	98	5.1	396	1 PER_DROPU			P91697 drosophila	
22	98	5.1	396	1 PER_DROPV			P91698 drosophila	
23	97	5.0	395	1 PER_DROEQ			P92203 drosophila	
24	96	5.0	390	1 PER_DROTP			P91716 drosophila	
25	95.5	4.9	283	1 PLCA_HUMAN			Q99943 h 1-acyl-sn	
26	95	4.9	308	1 PLSC_COCNU			Q43670 cocos nucif	
27	95	4.9	1093	1 PER_DROWI			Q03297 drosophila	
28	93	4.8	285	1 PLCA_MOUSE			Q35083 mus musculu	
29	93	4.8	428	1 YX10_BACSU			P42306 bacillus su	
30	92	4.8	397	1 NXF5_HUMAN			Q9h1b4 homo sapien	
31	91.5	4.7	384	1 UT1_MOUSE			Q8vhl0 mus musculu	
32	91.5	4.7	844	1 RRPO_IPNVS			P22174 infectious	
33	90	4.7	1679	1 YMF9_YEAST			Q04958 saccharomyc	

34	90	4.7	2103	1 RRPL_UUK	P33453 uukuniemi v
35	89.5	4.6	718	1 PLSB_CAEEL	Q22949 caenorhabdi
36	89	4.6	262	1 PLC1_CAEEL	Q93841 caenorhabdi
37	89	4.6	2832	1 NDVB_RHIME	P20471 rhizobium m
38	88.5	4.6	804	1 SYFB_BRUSU	Q8fxx4 brucella su
39	88.5	4.6	920	1 NML7_MYCTU	P96289 mycobacteri
40	88.5	4.6	1099	1 CYA7_MOUSE	P51829 mus musculu
41	88	4.5	979	1 Y064_MYCTU	O53609 mycobacteri
42	88	4.5	979	1 Y065_MYCBO	Q7u2x8 mycobacteri
43	87.5	4.5	804	1 SYFB_BRUME	Q8ye74 brucella me
44	87.5	4.5	857	1 I2C1_MOUSE	Q8cjg1 mus musculu
45	87	4.5	336	1 PYRD_VIBVU	Q8d9g5 vibrio vuln

ALIGNMENTS

RESULT 1  
PLCC\_HUMAN  
ID PLCC\_HUMAN STANDARD; PRT; 376 AA.  
AC Q9NRZ7; Q9NRZ6;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE 1-acyl-sn-glycerol-3-phosphate acyltransferase gamma (EC 2.3.1.51) (1-  
AGP acyltransferase 3) (1-AGPAT 3) (lysophosphatidic acid  
acyltransferase-gamma) (LPAAT-gamma) (1-acylglycerol-3-phosphate O-  
acyltransferase 3).  
GN AGPAT3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS GAMMA-1 AND GAMMA-2).  
RA Leung D.W.;  
RT "Structure and functions of lysophosphatidic acid acyltransferases.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fetal liver;  
RA Nagamine K., Kudoh J., Minoshima S., Kawasaki K., Hase T.,  
RA Shimizu N.;  
RT "Isolation of a novel gene encoding 1-acylglycerol-3-phosphate  
O-acyltransferase 3 (AGPAT3) from the human chromosome 21q22.3.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
CC -!- FUNCTION: Converts lysophosphatidic acid (LPA) into phosphatidic  
acid by incorporating acyl moiety at the 2 position (By  
similarity).



Best Local Similarity 31.6%; Pred. No. 5.8e-41;		
Matches 114;	Conservative 94;	Mismatches 148; Indels 5; Gaps 4;
QY	15 LFFASGLLVNLIQAI	CVVVVPVSKSLYRRINRVVAELLWLELVWLDWMAGVKVQIFTD 74
DB	20 VFIASGLLIINTIQ-LFTLLLPINKQLFRKINCRLSYCISSQLVMLLEWWSGTECTIFTD 78	
QY	75 HETFRLMGKEHALVISNHRSDIDWLGVWSAQRSGCLGSTLAVMKSSKFLPVIWGSMMWF 134	
DB	79 PRAYLKYGKENAIVLNLHKFEIDFLCGWSLSERFGLGGSKVLAKKELAYVPIIGMMWYF 138	
QY	135 SEYLFLEERSWAKDESTLKSIGIQRLSDFFPLFPWLALFVEGTRFTQAKLLAAQEVATSTGLP 194	
DB	139 TEMVFCSRKWEQDRKTVAATSLQHLRDYPEKYFFLIHCEGTRFTEKKHEISMQVARAKGLP 198	
QY	195 VPRNVLIPTKGFVS	AVSHMRSFVPAIYDVTVAIPKSSPAPIMLRLEKQPSVVVHVHIKR 254
DB	199 RLKHHLLPRTKGFATVRS	LRNVVS
QY	255 HLMKELPDTDEAVAQWCRDI	FVAKDALLDKHMAEGTFS
DB	258 IPLEDIPEDDDDECSAWLHKLYQEKDAFQEEYRTGTFFETPMVPPRRP-WTLVNWLFWAS 316	
QY	315 LVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSERSNP	AKIVPAKSKN 374
DB	317 LVLYPPFFQFL--VSMIRSGSSLTLASFILVFFVASVGVRRMIGVTEIDKGSAYGNSDSKQ 374	
QY	375 K	375
DB	375 K	375

```

RESULT 3
PLCD_RAT
ID      PLCD_RAT      STANDARD;      PRT;      378 AA.
AC      Q924S1;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      1-acyl-sn-glycerol-3-phosphate acyltransferase delta (EC 2.3.1.51) (1-
DE      AGP acyltransferase 4) (1-AGPAT 4) (lysophosphatidic acid
DE      acyltransferase-delta) (LPAAT-delta) (1-acylglycerol-3-phosphate O-
DE      acyltransferase 4).
DE      AGPAT4.
GN      Rattus norvegicus (Rat).
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Li W., Suzuki T.;
RT      "Rattus norvegicus mRNA for lysophosphatidic acid
RT      acyltransferase-delta, complete cds.";
RL      Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC      -!- FUNCTION: Converts lysophosphatidic acid (LPA) into phosphatidic
CC      acid by incorporating acyl moiety at the 2 position (By
CC      similarity).
CC      -!- CATALYTIC ACTIVITY: Acyl-CoA + 1-acyl-sn-glycerol 3-phosphate =
CC      CoA + 1,2-diacyl-sn-glycerol 3-phosphate.
CC      -!- PATHWAY: De novo phospholipid biosynthesis; second step.
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC      -!- SIMILARITY: Belongs to the 1-acyl-sn-glycerol-3-phosphate
CC      acyltransferase family.
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EMBL; AB067572; BAB62290.1; -.

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[illegible]

RESULT 4

PLCE_HUMAN	STANDARD;	PRT;	364 AA.
ID	PLCE_HUMAN		
AC	Q9NUQ2; Q81Z47; Q9BQG4;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	10-OCT-2003 (Rel. 42, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	1-acyl-sn-glycerol-3-phosphate acyltransferase epsilon (EC 2.3.1.51)		
DE	(1-AGP acyltransferase 5) (1-AGPAT 5) (lysophosphatidic acid		
DE	acyltransferase-epsilon) (LPAAT-epsilon) (1-acylglycerol-3-phosphate		
DE	O-acyltransferase 5).		
GN	AGPAT5.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Leung D.W.;		
RT	"Cloning and expression of LPAAT-epsilon.";		
RL	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Cohen D., Chumakov I., Blumenfeld M., Bougueleret L.;		
RL	Patent number WO932644, 01-JUL-1999.		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Amygdala;		
RX	MEDLINE=21154917; PubMed=11230166;		
RA	Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,		
RA	Ansorge W., Boecker M., Bloecker H., Bauersachs S., Blum H.,		
RA	Lauber J., Dueterhoeft A., Beyer A., Koehrer K., Strack N.,		
RA	Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,		



QY 41 LYRINRVVAELLWLELVLDWAGVKVQIFTDHETFRMLGKEHALVISNHRSDIDWL 100  
 |||::  
 Db 46 LYQRVDRLYCVCVQNMLFFPENITGVQILLYGDLP----KNKENVIYLANHQSTVDWIV 101  
 ::||:  
 QY 101 GWTSAQRSGLGSTLAVMKSSKFLPVIGWSMWFSEY--LFLEERSWAKDESTLKSGIQL 158  
 :  
 Db 102 ADMLAARQDALGHVRVYLKDKLKWPLPLYGF--YFAQHGGIYVKRS AKENDKEMRSKLQSY 159  
 :  
 QY 159 SDFPLPFWALFVEGTRF--TQAKLL-AAQEYATSTGLVPVPRNVLI PRTKGFVS AVSHMR 215  
 :  
 Db 160 VNAGTPMYLVIFPEGTRYNATYTKLLSASQAFAAQRGLAVLKHVLTPRIKATHVAFDSMK 219  
 :  
 QY 216 SFVPAIYDVTVAIP-----KSSPAPTMLRLFKGQPSVVHVHIKRHLMKELPD TDEAVA 268  
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
 Db 220 SHLDAIYDVTVVYEGNEKGSKYSNPSPMTFLCKQCPKLHIHFDRIDRNEVP EEQEHMK 279  
 :  
 QY 269 QWC RDIFVAKDALL 282  
 :  
 Db 280 KWLHERFEIKDRLL 293  
 :

**RESULT 6**  
**YBP2\_YEAST STANDARD; PRT; 397 AA.**  
 AC P38226;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical 45.5 kDa protein in FAR1-TCM62 intergenic region.  
 GN YBR042C OR YBR0412.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288c;  
 RA Andre B.; Ziepleluch C., Hein C., Jauniaux J.-C., Urrestarazu A.,  
 RA Viissers S.;  
 RRL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.  
 CC -! SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -! SIMILARITY: Belongs to the 1-acyl-sn-glycerol-3-phosphate  
 CC acyltransferase family.  
 CC -----  
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 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
 CC or send an email to license@isb-sib.ch).  
 CC -----  
 DR EMBL; Z35911; CAA84984.1; -.  
 DR PIR; S45900; S45900.  
 DR GermOnline; 138585; -.  
 DR SGD; S0000246; YBR042C.  
 DR InterPro; IPR002123; Acyltransferase.  
 DR Pfam; PF01553; Acyltransferase; 1.  
 DR SMART; SM00563; PlsC; 1.  
 KW Hypothetical protein; Phospholipid biosynthesis; Transferase;  
 KW Acyltransferase; Transmembrane.  
 FT TRANSMEM 13 33 POTENTIAL.  
 FT TRANSMEM 58 78 POTENTIAL.  
 FT TRANSMEM 118 138 POTENTIAL.  
 FT TRANSMEM 377 397 POTENTIAL.  
 SQ SEQUENCE 397 AA; 45515 MW; 04CADD1247D98A8 CRC64;

Query Match 14.0%; Score 271; DB 1; Length 397;

Query Match 14.0%; Score 271; DB 1; Length 397;  
Best Local Similarity 24.6%; Pred. No. 3.9e-16;  
Matches 87; Conservative 72; Mismatches 122; Indels 72; Gaps 13



Db 13 VVVPGISLFFQGLILLFLQTY-----KTLRCNRDIRKQIGLNKTKRLFLVIVSS 65  
QY 60 LIDWAGVKVQIFTDHE-----TF-----RLMG--KEHALVISNHRSDIDWLVGVSA 105  
Db 66 ILHWVAPSAVRITTENSSVPKGTFFLDLKKRILSHLKSNSVAICNHQIYTDWIFLWLA 125  
QY 106 QRSGLGSLAVMKKSKFLPVGWMSWFSEYLFLEERSWAKDESTLKSGI----- 155  
Db 126 YTSNLGANVFILKKSLASIPILGFGMRNMFIFMSRKWAQDKITLSNLAGLDSNARGA 185  
QY 156 -----ORLSD-----PPLPFWLALFVEGTRFTQAKLLAAQEVATSTG 192  
Db 186 GSLAGKSPERITEEGESIWNPEVIDPKQIHPYNLILPPEGTNLSADTRQKSAKIAKIG 245  
QY 193 LPVPRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIP--KSSPAPTMLRLFKG-----Q 244  
Db 246 KKPFKNVLLPHSTGLRYSLOKLPKPSIESLYDITIGYSGVKQEEYGEIYGLKSFLEGGY 305  
QY 245 PSVVHVHVKRHLMKELPDDE-AVAQNCRDIFVAKDALLDKHMAEGTF-SDQE 295  
Db 306 PKLVDIHIRAFVDKIDPLEDENEFSEWLYKIWSEKDALMERYYSTGFSVSDPE 358

RESULT 7

YD18\_YEAST  
ID YD18\_YEAST STANDARD; PRT; 396 AA.  
AC Q12185;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Hypothetical 45.9 kDa protein in KCS1-GCV1 intergenic region.  
GN YDR018C OR YD9335.04C OR P2F396.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=S288c / AB972;  
RA Dedman K., Brown D., Hamlyn N., Bowman S., Barrell B.G.,  
RA Rajandream M.A.;  
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97051598; PubMed=8896275;  
RA Eide L.G., Sander C., Prydz H.;  
RT "Sequencing and analysis of a 35.4 kb region on the right arm of  
RT chromosome IV from Saccharomyces cerevisiae reveal 23 open reading  
RT frames.";  
RL Yeast 12:1085-1090(1996).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -!- SIMILARITY: Belongs to the 1-acyl-sn-glycerol-3-phosphate  
CC acyltransferase family.

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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL; Z74314; CAA98838.1; -  
DR EMBL; X95966; CAA65210.1; -  
DR EMBL; Z49770; CAA89843.1; -  
DR PIR; S54641; S54641.  
DR GeneOnline; 140509; -  
DR SGD; S0002425; YDR018C.  
DR InterPro; IPR002123; Acyltransferase.  
DR Pfam; PF01553; Acyltransferase; 1.  
DR SMART; SM00563; Plsc; 1.  
KW Hypothetical protein; Phospholipid biosynthesis; Transferase;

FT TRANSMEM 27 47 POTENTIAL.  
FT TRANSMEM 69 89 POTENTIAL.  
FT TRANSMEM 123 143 POTENTIAL.  
FT TRANSMEM 372 392 POTENTIAL.  
SQ SEQUENCE 396 AA; 45938 MW; 9F55AB56C8FD44DD CRC64;  
Query Match 12.8%; Score 247; DB 1; Length 396;  
Best Local Similarity 25.8%; Pred. No. 4.9e-14;  
Matches 85; Conservative 61; Mismatches 129; Indels 54; Gaps 11;  
QY 17 FASGLLVNLIQAICVYVVRPVSKSLYRR-INRVVAELLWLELVWLDWAGVKVQIFTDH 75  
Db 33 FISGSLSIIVVFQICQLVLLPWSKIRFQNGINQSKKAFIV-LCMILNMVAPSSLNV--TF 89  
QY 76 ETRFLMG-----KEHALVISNHRSDIDWLVGVSAQRSGLGSLTAVMKKSKF 124  
Db 90 ETSRPLKNSSNAKPCFRFKDRAIIIANHQMYADWIYLVWLSFVSNLGNVYIILKKALQY 149  
QY 125 LPVIGWMSWFSEYLFLEERSWAKDESTL-----KSGIQRLSDFPLP 164  
Db 150 IPLLGFGRNFKFIFLSRNWQKDEKALTNLSVMDLNARCKGPLTNYKSCYSKTNESIAA 209  
QY 165 FWLALFVEGTRF---TQAKLLAAQEVATSTGLPVRNVLIPRTKGFVSAVSHMRSFVPAI 221  
Db 210 YNLIMFPGTNSLTKTREKSEAFQRAHLHDVQL-RHLLPHSKGLKPAVEKLAPSLDAI 268  
QY 222 YDVTVAIPKSSPAP-----TMLRLF--KGQPSVVHVHVKRHLMKELP-DTDEAVAQ 269  
Db 269 YDVTIGY---SPALRTEYVGTFTLTKIFLMGVPEKVDYIREFRVNEIPLQDDVEFFN 325  
QY 270 WCRDIFVAKDALLDKHMAEGTFSDQELQD 298  
Db 326 WLLGVWKEKDQLLEDYNTGTGQFKSNKND 354

RESULT 8

Y205\_HUMAN  
ID Y205\_HUMAN STANDARD; PRT; 370 AA.  
AC Q92604;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Hypothetical protein KIAA0205.  
GN KIAA0205.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow;  
RX MEDLINE=97191544; PubMed=9039502;  
RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y.,  
RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;  
RT "Prediction of the coding sequences of unidentified human genes. VI.  
RT The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by  
RT analysis of cDNA clones from cell line KG-1 and brain.";  
RL DNA Res. 3:321-329(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,



```

[1]
RN      SEQUENCE FROM N.A.
RP      STRAIN=K12 / MG1655;
RC      MEDLINE=93347969; PubMed=8346018;
RX      Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.;
RA      "Analysis of the Escherichia coli genome. III. DNA sequence of the
RT      region from 87.2 to 89.2 minutes.";
RL      Nucleic Acids Res. 21:3391-3398(1993).
CC      -!- SIMILARITY: Belongs to the 1-acyl-sn-glycerol-3-phosphate
CC      acyltransferase family.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; L19201; AAB02997.1; -.
DR      EMBL; AE000461; AAC76850.1; -.
DR      PIR; S40808; S40808.
DR      EcoGene; EG11833; yihG.
DR      InterPro; IPR002123; Acyltransferase.
DR      Pfam; PF01553; Acyltransferase; 1.
DR      SMART; SM00563; Plsc; 1.
DR      Hypothetical protein; Complete proteome.
SQ      SEQUENCE 310 AA; 36289 MW; 9F8E3F52EB0E186E CRC64;

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	Query Match	7.6%; Score 148; DB 1; Length 310;
	Best Local Similarity	21.6%; Pred.No. 1.6e-05;
Matches	71; Conservative	58; Mismatches 115; Indels 84; Gaps 14;
Qy	6 AAVVPLGLLFFASGILLVNLIQAICYV--VVRPVYSKSL-----YRRINRVVAELLWLEL	57    ::: :: ::  :: ::
Dd	15 AAITLLLSI-----VLTIIVTIFCSVPILIIAGIVKLPLLPPVIWRKVSRFCDFMYC--	66    ::: :: ::  :: ::
Qy	58 VWLIDWWAGVKVOIFTD-----HETFRIMGKEHALVISNHRSDIDLWVGWSAQSGC	110    ::: :: ::  :: ::
Dd	67 -----WCEGLA VLLHLNPHQLQWEVHGLEGSKKNWYLICNRHSWADIVLCVLFPRKH--	119    ::: :: ::  :: ::
Qy	111 LGSTLA VMKKSSFLPVI GWSMWFSEYLFLE R-----SWAKDESTLKSGIQRLS	159 :   ::: :: ::  :: ::
Dd	120 IPMKYF LKQOLA WPF FLGLACWSLDMPFMKRYSA YLLRHPERRCKDVETTRRSCEK--	177 :   ::: :: ::  :: ::
Qy	160 DFPL-PFWLALFVEGRFTQAKLLAAQEYATSTGLPVP RNVLIRPTKGFS AVSHMSFV	218    ::: :: ::  :: ::
Dd	178 -FRLHPTTVNFEGSRFTQEK--HQO THSTF-----QNLLPPKAAGIAMALNVLGKQF	228    ::: :: ::  :: ::
Qy	219 PAIYDVTVAIPKSSAPTMLRLF KGPSVVHVHI-----KRHLMKE	259 :   ::: :: ::  :: ::
Dd	229 DKLLNV TLCYPDN NRQP-FFDMLS GLTRI VHVDLP IADELHG DYINDKS FKRHFQ--	285 :   ::: :: ::  :: ::
Qy	260 LPDTDEAVA QWC RDIFV AKDAL LD KHMA	287    ::: :: ::  :: ::
Dd	286 -----QWLNSLWQ EKDR LLT SLMS	304    ::: :: ::  :: ::

```

RESULT 10
YT73 CAEEL
ID YT73 CAEEL STANDARD; PRT; 391 AA.
AC Q11087;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 44.7 kDa protein COLC10.3 in chromosome X.
GN COLC10.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.

```

RESULT 9			
ID	YIHG ECOLI	STANDARD;	PRT; 310 AA.
AC	P32129;		
DT	01-OCT-1993 (Rel. 27, Created)		
DT	01-OCT-1993 (Rel. 27, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Hypothetical protein yihG.		
GN	YIHG OR B3862.		
OS	Escherichia coli.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;		
OC	Enterobacteriaceae; Escherichia.		
OX	NCBI TaxID=562;		

---

ID	YH73_CAEEL	STANDARD;	PRT; 391 AA.
AC	Q11087;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	01-NOV-1997 (Rel. 35, Last annotation update)		
DE	Hypothetical 44.7 kDa protein C01C10.3 in chromosome X.		
GN	C01C10.3.		
OS	Caenorhabditis elegans.		
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;		
OC	Rhabditidae; Peloderinae; Caenorhabditis.		
OX	NCBI_TaxID=6239;		
RN	[1]		
RP	SEQUENCE FROM N.A.		







DE 1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) (1-AGP  
DE acyltransferase) (1-AGPAT) (Lysophosphatidic acid acyltransferase)  
DE (LPAAT).  
GN PLSC.  
OS Limnanthes douglasii (Douglas's meadowfoam).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Brassicales; Limnanthaceae; Limnanthes.  
OX NCBI\_TaxID=28973;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96028122; PubMed=7588719;  
RA Hanke C., Wolter F.P., Coleman J., Peterek G., Frentzen M.;  
RT "A plant acyltransferase involved in triacylglycerol biosynthesis  
RT complements an Escherichia coli sn-1-acylglycerol-3-phosphate  
RT acyltransferase mutant.";  
RL Eur. J. Biochem. 232:806-810 (1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96046746; PubMed=7579178;  
RA Brown A.P., Brough C.L., Kroon J., Slabas A.R.;  
RT "Identification of a cDNA that encodes a 1-acyl-sn-glycerol-3-  
RT phosphate acyltransferase from Limnanthes douglasii.";  
RL Plant Mol. Biol. 29:267-278 (1995).  
CC -!- FUNCTION: Converts lysophosphatidic acid (LPA) into phosphatidic  
CC acid by incorporating acyl moiety at the 2 position. This enzyme  
CC uses erucoyl-CoA as an acyl donor.  
CC -!- CATALYTIC ACTIVITY: Acyl-CoA + 1-acyl-sn-glycerol 3-phosphate =  
CC CoA + 1,2-diacyl-sn-glycerol 3-phosphate.  
CC -!- PATHWAY: De novo phospholipid biosynthesis; second step.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -!- SIMILARITY: Belongs to the 1-acyl-sn-glycerol-3-phosphate  
CC acyltransferase family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
DR EMBL; X83266; CAA58239.1; -.  
DR EMBL; Z46836; CAA86877.1; -.  
DR PIR; S60477; S60477.  
DR InterPro; IPR002123; Acyltransferase.  
DR InterPro; IPR004552; AGP acyltrn.  
DR Pfam; PF01553; Acyltransferase; 1.  
DR SMART; SM00563; PlsC; 1.  
DR TIGRfams; TIGR00530; AGP acyltrn; 1.  
KW Phospholipid biosynthesis; Transferase; Acyltransferase;  
KW Transmembrane.  
FT TRANSMEM 40 60 POTENTIAL.  
FT TRANSMEM 71 91 POTENTIAL.  
FT TRANSMEM 110 130 POTENTIAL.  
FT CONFLICT 46 I -> V (IN REF. 2).  
FT CONFLICT 188 R -> G (IN REF. 2).  
FT CONFLICT 262 V -> I (IN REF. 2).  
FT CONFLICT 281 N -> K (IN REF. 2).  
SQ SEQUENCE 281 AA; 31716 MW; 9C880BD9E492EE2A CRC64;

Query Match 6.1%; Score 118.5; DB 1; Length 281;  
Best Local Similarity 21.7%; Pred. No. 0.0055;  
Matches 56; Conservative 46; Mismatches 79; Indels 77; Gaps 12;

QY 29 ICYVWRPVSKSLYRRINRVVAELLW-----LELVW-----LIDWAG 66  
Db 42 VCFAIV-----LITAVAWGLIMVLLLPYPMRIRLGNLYGHIIGGLVVIY 88

QY 67 VKVQIFTDHFRLMGKEHALVISNHRSDID-WLVGWVSAQRSGCLGSLAVMKSKFL 125  
Db 89 IPIKIQGSEHT-----KKRAIYISNHASPIDAFFVMWLP-----IG-TVGVAKEVIWY 137

QY 126 PVIGSMWFSEYLFLEERS-WAKDESTLKSGIQRLSDFFPLPFWLALFVEGTRFTQAKLLAA 184  
Db 138 PLLGQLYTLAHHIRIDRSNPAAAIQSMKEAVRVITEKNLS--LIMFPEGTRSRDGRLLPF 195  
QY 185 QE-----YATSTGLPVRNVL-----IPRTKGFVS-----AVSHMRSF 217  
Db 196 KKGFFVHLALQSHLPVIVPMILTGTHLAWRKGTFRVRVPVITVKYLPPIINTDDTVDKIDDY 255  
QY 218 VPAIYDVTVVAIPKSSPAP 235  
Db 256 VKMIHDVYVVRNLPASQKP 273

Search completed: July 7, 2004, 13:40:19  
Job time : 20 secs





OM protein - protein search, using sw model

Run on: July 7, 2004, 13:37:33 ; Search time 21 Seconds  
(without alignments)  
1726.867 Million cell updates/sec

Title: US-09-914-098-56  
Perfect score: 1935  
Sequence: 1 MAIAAAAVVPLGLFFASG.....QSERSNPAKIVPAKSNKGS 377

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1519	78.5	377	S60478	probable 1-acyl-sn
2	1450.5	75.0	374	S52645	probable 1-acyl-gl
3	1277	66.0	376	D96550	hypothetical prote
4	1161.5	60.0	310	T06755	probable glycerol-
5	1156.5	59.8	311	T07936	probable glycerol-
6	414	21.4	393	B96780	hypothetical prote
7	310.5	16.0	350	T40466	probable acetyltra
8	287	14.8	344	T31913	hypothetical prote
9	271	14.0	397	S45900	probable membrane
10	269	13.9	918	T34057	hypothetical prote
11	250	12.9	439	T22689	hypothetical prote
12	247	12.8	396	S54641	probable membrane
13	240.5	12.4	523	T25998	hypothetical prote
14	160.5	8.3	304	B83541	probable polynucle
15	148	7.6	310	S40808	polynucleotide ade
16	148	7.6	310	A91227	probable endonucle
17	148	7.6	310	G86073	probable endonucle
18	131.5	6.8	295	B83587	probable polynucle
19	129	6.7	302	AI0950	probable acyltrans
20	127	6.6	294	D82371	probable polynucle
21	124.5	6.4	391	T15366	hypothetical prote
22	121	6.3	303	A48600	probable sn2-acylg
23	120	6.2	225	B45582	probable 1-acylgly
24	120	6.2	245	S20460	1-acylglycerol-3-p
25	120	6.2	245	AE0888	1-acyl-glycerol-3-
26	119	6.1	279	T50125	probable 1-acylgly
27	117.5	6.1	281	S60477	1-acylglycerol-3-p
28	115.5	6.0	240	D64089	1-acylglycerol-3-p
29	115.5	6.0	363	T20608	hypothetical prote

1-acyl-sn-glycerol  
1-acyl-sn-glycerol  
1-acylglycerol-3-p  
hypothetical prote  
probable acyltrans  
probable 1-acylgly  
1-acyl-sn-glycerol  
1-acylglycerol-3-p  
1-acylglycerol-3-p  
hypothetical prote  
transcription elon  
2-acylglycerophosp  
probable 1-acygly  
1-acylglycerol-3-p  
conserved hypothet

ALIGNMENTS

RESULT 1

S60478  
probable 1-acyl-sn-glycerol-3-phosphate acyltransferase - Limnanthes douglasii  
C;Species: Limnanthes douglasii  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 17-Mar-2000  
C;Accession: S60478  
R;Brown, A.P.; Brough, C.L.; Kroon, J.T.M.; Slabas, A.R.  
Plant Mol. Biol. 29, 267-278, 1995  
A;Title: Identification of a cDNA that encodes a 1-acyl-sn-glycerol-3-phosphate acyltra:  
A;Reference number: S60477; MUID:96046746; PMID:7579178  
A;Accession: S60478  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-377 <BRO>  
A;Cross-references: EMBL:Z48730; NID:g1067137; PIDN:CAA88620.1; PID:g1067138  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1995  
C;Superfamily: probable membrane protein YBR042c

Query Match 78.5%; Score 1519; DB 2; Length 377;  
Best Local Similarity 77.0%; Pred. NO. 1.5e-124;  
Matches 282; Conservative 43; Mismatches 41; Indels 0; Gaps 0;

Qy 1 MAIAAAAVVPLGLFFASGLLVNLIOAICYVVVRPVSKSLYRINRVVAELLWLELWL 60  
Db 1 MAIPAAAFIVPISLLFFMSGVLVNFIOAVFYVLRVPISKDYRINTLVAEELLWLELVV 60  
Qy 61 IDWAGVKVQIFDTHETERLMGKEHALVISNHRSDIDWLGVWVSAQRSGLGSLTAVMKK 120  
Db 61 IDWAGVKVQLYTDTESFRLMGKEHALLICNHRSDIDWLIGWLAQRGCLSSSIAMVKK 120  
Qy 121 SSKFLPVGWSMWFSEYLFLEERSNAKDESTLKSGIQRLSDFFPLPFWLALFVEGTRFTQAK 180  
Db 121 SSKFLPVGWSMWFSEYLFLEERNWAKDENTLKSGIQRLNDFPKPFWLALFVEGTRFTKAK 180  
Qy 181 LLAQAEYATSTGLPVRPNVLIPTKGFVSAVSHMESFVPAIYDVTVAIPKSSPAPTMLRL 240  
Db 181 LLAQAEYAAASAGLPVRPNVLIPTKGFVSAVSNMRSFVPAIYDLTVAIPKTEQPTMLRL 240  
Qy 241 FXGQPSVVHVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDDQELDTG 300  
Db 241 FRGKSSVVHVHLKRHLMKDLPKTDDGVAQWCKDQFISKDALLDKHVAEDTFSGLEVDIG 300  
Qy 301 RPIKSLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIOFSQSE 360  
Db 301 RPKMSLVVVVSWMCLLCGLVKFLQWSALLSSWKGMWMTTFVLGIVTVLMHILIRSSQSE 360  
Qy 361 RSNPAK 366  
Db 361 HSTPAK 366

RESULT 2

S52645  
probable 1-acyl-glycerol-3-phosphate acyltransferase - maize  
C;Species: Zea mays (maize)  
C;Date: 14-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 19-May-2000  
C;Accession: S52645  
R;Brown, A.P.; Coleman, J.; Tommey, A.M.; Watson, M.D.; Slabas, A.R.  
Plant Mol. Biol. 26, 211-223, 1994  
A;Title: Isolation and characterisation of a maize cDNA that complements a 1-acyl sn-gly  
her acyltransferases.  
A;Reference number: S52645; MUID:95035993; PMID:7948871  
A;Accession: S52645  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-374 <BRO>  
A;Cross-references: EMBL:229518; NID:G575959; PIDN:CAA82638.1; PID:G575960  
C;Superfamily: probable membrane protein YBR042C

Query Match 75.0%; Score 1450.5; DB 2; Length 374;  
Best Local Similarity 70.7%; Pred. NO. 1.4e-118;  
Matches 265; Conservative 51; Mismatches 58; Indels 1; Gaps 1;

QY 1 MAIAAAVVPVPLGLLFFASGLLVNLIQAICYVWVRPVSKSLYRRINRVVAELLWLELWVL 60  
Db 1 MAIPLVVLPVPLGLLFFASGLLVNLIQAICYVWVRPVSKSLYRRINRVVAELLWLELWVL 60

QY 61 IDWAGVKVQIFTDHETFRMLGKEHALVISNHRSDIDWLVGWVSAQSGCLGSLTAVMKK 120  
Db 61 VDWAGVKVQLHADEETVRSMGKEHALVISNHRSDIDWLVGWVSAQSGCLGSLTAVMKK 120

QY 121 SSKFLPVIGSMWFESEYLFERSWAKDESTLKSIGIQLSDPFLPFWLALFVEGTRFTQAK 180  
Db 121 SSKFLPVIGSMWFESEYLFERSWAKDESTLKSIGIQLSDPFLPFWLALFVEGTRFTQAK 180

QY 121 SSKFLPVIGSMWFESEYLFERSWAKDESTLKSIGIQLSDPFLPFWLALFVEGTRFTQAK 180  
Db 121 SSKFLPVIGSMWFESEYLFERSWAKDESTLKSIGIQLSDPFLPFWLALFVEGTRFTQAK 180

QY 181 LAAQEVATSTGLPVRNVLPRTKGFVSAVSHMRSPFPAIYDVTVAIPKSSPAPTMLRL 240  
Db 181 LAAQEVATSTGLPVRNVLPRTKGFVSAVSHMRSPFPAIYDVTVAIPKSSPAPTMLRL 240

QY 241 FKQPSVVHVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDELDQDTG 300  
Db 241 LKGQSSVHVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDELDQDTG 300

QY 301 RPIKSLLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE 360  
Db 300 RPKVSLLVTLFWSCLLFGAIEFFKWTQLLSTWRGVAFSAFGLAVVTALMQILIQFSQSE 360

QY 361 RSNPAKIVPAKSKNK 375  
Db 360 RSSSARAARNRVKKE 374

RESULT 3  
D96550  
hypothetical protein F11M15.12 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 01-Mar-2002  
C;Accession: D96550  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: D96550  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-376 <STO>

A;Gene: F11M15.12  
A;Map position: 1  
C;Superfamily: probable membrane protein YBR042C

Query Match 66.0%; Score 1277; DB 2; Length 376;  
Best Local Similarity 62.3%; Pred. NO. 1.8e-103;  
Matches 228; Conservative 62; Mismatches 76; Indels 0; Gaps 0;

QY 1 MAIAAAVVPVPLGLLFFASGLLVNLIQAICYVWVRPVSKSLYRRINRVVAELLWLELWVL 60  
Db 1 MKIPAALVFPVGVFLISGLIVNIIQLVFFIIVRPFSRLYRRINRVVAELLWLELWVL 60

QY 61 IDWAGVKVQIFTDHETFRMLGKEHALVISNHRSDIDWLVGWVSAQSGCLGSLTAVMKK 120  
Db 61 FDWACIKINLYVDAETLELIGKEHALVISNHRSDIDWLVGWVMAQVRGCLGSSLAIMKK 120

QY 121 SSKFLPVIGSMWFESEYLFERSWAKDESTLKSIGIQLSDPFLPFWLALFVEGTRFTQAK 180  
Db 121 EAKYLPVIGSMWFESEYLFERSWAKDESTLKSIGIQLSDPFLPFWLALFVEGTRFTQAK 180

QY 181 LAAQEVATSTGLPVRNVLPRTKGFVSAVSHMRSPFPAIYDVTVAIPKSSPAPTMLRL 240  
Db 181 LAAQEVATSTGLPVRNVLPRTKGFVSAVSEIRSPFPAIYDCTLTVHNNQPTTLRLM 240

QY 241 FKQPSVVHVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDELDQDTG 300  
Db 241 FSGQSSVHVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDELDQDTG 300

QY 301 RPIKSLLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE 360  
Db 301 RPIKPLVIVIIWLGFLVGGFKLLQWLSIVASWKIILLFVFFLVIAITMTQILIQSSSQ 360

QY 361 RSNPAK 366  
Db 361 RSTPAK 366

RESULT 4  
T06755  
probable glycerol-3-phosphate O-acyltransferase (EC 2.3.1.15) - Arabidopsis thaliana  
N;Alternate names: protein F15B8.160  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 19-May-2000  
C;Accession: T06755  
R;Quetier, F.; Benes, V.; Rechmann, S.; Borkova, D.; Ansoorge, W.; Salanoubat, M.; Mewes,  
submitted to the Protein Sequence Database, April 1999  
A;Reference number: Z15794  
A;Accession: T06755  
A;Molecule type: DNA  
A;Residues: 1-310 <QUE>  
A;Cross-references: EMBL:AL049660; GSPDB:GN00061; ATSP:F15B8.160  
A;Experimental source: cultivar Columbia; BAC clone F15B8  
C;Genetics:  
A;Gene: ATSP:F15B8.160  
A;Map position: 3  
A;Introns: 26/3; 46/3; 72/3; 125/3; 167/3; 198/3; 227/3  
C;Superfamily: probable membrane protein YBR042C  
C;Keywords: acyltransferase; coenzyme A

Query Match 60.0%; Score 1161.5; DB 2; Length 310;  
Best Local Similarity 61.3%; Pred. NO. 1.6e-93;  
Matches 228; Conservative 30; Mismatches 35; Indels 79; Gaps 1;

QY 3 IAIAAVVVPVPLGLLFFASGLLVNLIQAICYVWVRPVSKSLYRRINRVVAELLWLELWVL 62  
Db 2 VIAAAVIVPLGLLFFISGLVNLNLF----- 25

QY 63 WWAGVKVQIFTDHETFRMLGKEHALVISNHRSDIDWLVGWVSAQSGCLGSLTAVMKKSS 122  
Db 26 -----ORSGCLGSALAVMKKSS 42

Db 43 KFLPVI GSWMFSEYLFLE RNWAKDESTL KSGLQRLSDP RPFWLALFVEGTRFT EAKLK 102

Qy 183 AAQEYATSTGLPVPRNVLI PRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLR LFK 242

Db 103 AAQEYAAASSELPIPRNVLI PRTKGFVSAVSNMRSFVPAIYDVTVAIPKTSPPPTMLR LFK 162

Qy 243 QGPSVVHVHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFS DQELQDTGRP 302

Db 163 QGPSVVHVHIKCHSMKDLPESDDAIAQWCRDQFVAKDALLDKHIAADTFPGQEQE NIGRP 222

Qy 303 IKSLLVTVSWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQS ERS 362

Db 223 IKSLAVVLSWACVLTGLAIKFLHWAQLFSSWKGITISALGLGIITLCMQILIRSSQS ERS 282

Qy 363 NPAKIVPAKSKN 374

Db 283 TPAKVVPAPKPD 294

RESULT 5

T07936

probable glycerol-3-phosphate O-acyltransferase (EC 2.3.1.15) - rape

N:Alternate names: 1-acyl-sn-glycerol-3-phosphate acyltransferase

C:Species: Brassica napus (rape)

C:Date: 21-May-1999 #sequence\_revision 21-May-1999 #text\_change 20-Jun-2000

C:Accession: T07936

R:Brough, C.L.

submitted to the EMBL Data Library, June 1995

A:Reference number: Z16230

A:Accession: T07936

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-311 <BRO>

A:Cross-references: EMBL:Z49860; NID:g1149594; PIDN:CAA90019.1

A:Experimental source: cv. jet neuf; embryo

C:Superfamily: probable membrane protein YBR042c

C:Keywords: acyltransferase; coenzyme A

Query Match 59.8%; Score 1156.5; DB 2; Length 311;

Best Local Similarity 61.4%; Pred. No. 4.5e-93;

Matches 227; Conservative 33; Mismatches 31; Indels 79; Gaps 1;

Qy 5 AAAVVVPLGLLFFASGLLVNLIQAICYVVVVRPVSKSLYRINRVVAELLWLELV LIDW 64

Db 4 AA AVIPLGI LFFISGLVNL----- 25

Qy 65 AGVKVQIFTDHTFRLMGKEHALVISNHRSDIDWLGVWSAQRSGCLGSTLAVMKSKSF 124

Db 26 -----QRSGLGSALAVMKSKSF 44

Qy 125 LPVIGWSMWFSEYLFLE RSWAKDESTL KSGIQR LSDFP LFPWLALFVEGTRFTQAKLLAA 184

Db 45 LPVIGWSMWFSEYLFLE RNWAKDESTL KSGLQRLNDP RPFPWLALFVEGTRFT EAKLKAA 104

Qy 185 QEYATSTGLPVPRNVLI PRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLR LFKGQ 244

Db 105 QEYAAASSELPIPRNVLI PRTKGFVSAVSNMRSFVPAIYDVTVAIPKTSPPPTMLR LFKGQ 164

Qy 245 PSVVHVHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFS DQELQDTGRPIK 304

Db 165 PSVVHVHIKCHSMKDLPESEDEIAQWCRDQFVTKDALLDKHIAADTFAGQKEQNIGRPIK 224

Qy 305 SLLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQS ERSNP 364

Db 225 SLAVVLSWACLLTGLAMKFLHWSNLFSSWKGIALSALGLGIITLCMQILIRSSQS ERSSTP 284

Qy 365 AKIVPAKSKN 374

Db 285 AKVAPAKPKD 294

RESULT 6

B96780

hypothetical protein F9E10.13 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

C:Accession: B96780

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: B96780

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-393 <STO>

A:Cross-references: GB:AE005173; NID:g6646762; PIDN:AAF21074.1; GSPDB:GN00141

C:Genetics:

A:Gene: F9E10.13

A:Map position: 1

Query Match 21.4%; Score 414; DB 2; Length 393;

Best Local Similarity 34.2%; Pred. No. 3.1e-28;

Matches 106; Conservative 52; Mismatches 132; Indels 20; Gaps 6;

Qy 9 VVPLGLLFFASGLLVNLIQAICYVVVVRPVSKSLYRRI-----NRVVAEL---LWLEL-VW 59

Db 17 LTPRLRLGLMILLVFLSTAFMFLLYFAPIAALGLRLLSVQOSRKVSVSLIFGLWLALWPY 76

Qy 60 LIDWAGVKVQIFTDHTFRLMGKEHALVISNHRSDIDWLGVWSAQRSGCLGSTLAVMK 119

Db 77 LFTVNGTTTVFSGD---IIPVEKRVLLIANHRTEVDMVLMNIALRKGCGLGYIKYVLK 132

Qy 120 KSKFELPVIGWSMWFSEYLFLE RSWAKDESTL KSGIQR LSDFP LFPWLALFVEGTRFTQA 179

Db 133 SSLMKLPIFGWGFHVLEFIPVERKREVDEPVLQLQMLSSFKDPQEP LWLALFP EGTDTFTEE 192

Qy 180 KLLAAQEYATSTGLPVPRNVLI PRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLR 239

Db 193 KCKRSQKFAAEVGLPALSNVLLPKTRGFGVCLEVLHNSLDVAVDLTIA YKPCPS-FMDN 251

Qy 240 LFKQPSVVHVHIKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFS DQELQDT 299

Db 252 VFGTDPSEVHIHVRVRLKKEIPANEAEBSAWLMDSFKLKDKLLSDFN AQGKFNQ----- 306

Qy 300 GRPIKSLLVV 309

Db 307 -RPEELSVL 315

RESULT 7

T40466

probable acetyltransferase protein - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 01-Mar-2002

C:Accession: T40466

R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Baker, S.; Mungall, K.

submitted to the EMBL Data Library, November 1998

A:Reference number: Z21931

A:Accession: T40466

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-350 <LYN>

A:Cross-references: EMBL:AL034382; PIDN:CAA22289.1; GSPDB:GN00067; SPDB:SPBC428.14

A:Experimental source: strain 972h-; cosmid c428

C:Genetics:

A:Gene: SPDB:SPBC428.14

A:Map position: 2

C:Superfamily: probable membrane protein YBR042c

Query Match 16.0%; Score 310.5; DB 2; Length 350;  
Best Local Similarity 27.1%; Pred. No. 2.8e-19;  
Matches 84; Conservative 62; Mismatches 133; Indels 31; Gaps 8;  
QY 37 VSKSLYRR---INRWVAELLWLELWLDWAGVKVQIFTDHETFRL-----MG 82  
Db 36 VNKELYNKIYIAFTKSFAGILFTALVQL---FSPTPTVLTLYDPELRNLFYLDNRGCLLETIA 92  
QY 83 KEHALVISNHRSDIDWLVGWSAQRSGCLGSTLAVMKKSKFPLPVIGWSMWFSEYLFLE 142  
Db 93 AERNIVIANHQLYSDWYVWMLSYTAKQHGHHVIMLNKSLKWLPLVIGWGMQLFRFIFLSR 152  
QY 143 SWAKDESTLXSGIQRLSDPFLPFWLALFVEGTRFTQAKLLAAQEAATSTGLPVPRNVLP 202  
Db 153 KWDKDYETMSRHHKFIKRVNDRDSVSLILPPEGTNLVESTYQSRVYADKIGVKMPKHLMLP 212  
QY 203 RTKGFVSASHMRSFVPAIYDVTVAIPKSSP-----APTMLRL-FKQOP-SVHVHVIKR 254  
Db 213 RVRLGFLYSQRLDSMTYLYDYTFYFSDPSPKKYAADAFSLPKLFFEGVPIKRLHIHVR 272  
QY 255 HLMKELPDTEAVAQWCRDIFVAKDALLDKHMAEGTSDQELQDTGSPKSLVVIS--- 311  
Db 273 FPISEIPTBEDQFTDLYQVWYERKLDITLLETGNFPGPKLHTTVRLKRLHLEILSLS 332  
QY 312 --WACLVVAG 319  
Db 333 VLFTC-IVAG 341

RESULT 8  
T31913  
hypothetical protein T05H4.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
C:Accession: T31913  
R:Blanchard, M.  
Submitted to the EMBL Data Library, July 1997  
A:Description: The sequence of C. elegans cosmid T05H4.  
A:Reference number: Z21097  
A:Accession: T31913  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-344 <BLA>  
A:Cross-references: EMBL:AF016452; PIDN:AAB66008.1; GSPDB:GN00023; CESP:T05H4.1  
A:Experimental source: strain Bristol N2; clone T05H4  
C:Genetics:  
A:Gene: CESP:T05H4.1  
A:Map position: 5  
A:Introns: 55/3; 212/1; 243/3; 298/3

Query Match 14.8%; Score 287; DB 2; Length 344;  
Best Local Similarity 26.7%; Pred. No. 3e-17;  
Matches 92; Conservative 64; Mismatches 157; Indels 32; Gaps 12;  
QY 14 LFFASGLLVNLIQAICYVVRPVSKSLYRR-INRWVAELLWLEL-VWLIDWAGVKVQI 71  
Db 11 VLVFFSLLGTGTVLLPPLIPLAWFAPKLWRTCADRLVG--FWLTFPCSLIEWFGV--- 64  
QY 72 FTDHETFRMLG-----KEHALVISNHRSDIDWLVGWSAQRSG--CLGSTLAVMKKSKF 124  
Db 65 -----NFRVTGDLIERDEPAIIMNHRTRLDWLFWSNALYKMDPWLTTTEKISLKA 119  
QY 125 LPVIGWSMWFSEYLFERSWAKDESTLKSQIRLSDPFLPFWLALFVEGTRFTQAKLLAA 184  
Db 120 IPGAGWAMSSGSYIFLDNRNFENDKPVLERIVKYSGSEKKYQILLFAEGTDKGERATRLS 179  
QY 185 QEYATSTGLPVPRNVLPRTKGFVSASHMR--SFVPAIYDVTVAIPKSSPAPTMRLFLX 242  
Db 180 DAFADKNGLPREYVYVLPRTTGFKFLMELMKENYIKYVYDLTIAY-SGTIVDTAKLLA 238  
QY 243 GQ-PSVVHVIKRLHLMKELPDTEAVAQWCRDIFVAKDALLDK-----HMAEGTSDQEL 296

QY 297 QDTGRPIKSLLVVISW--ACLIWAGSVKFLQWSSLLSSWKGVAFS 339  
Db 298 PETTTGIGYVAFAFWVLASLIWMGAIYSLLWVKVINRFGDCYS 342  
RESULT 9  
S45900  
probable membrane protein YBR042c - yeast (Saccharomycetes cerevisiae)  
N:Alternate names: hypothetical protein YBR0412  
C:Species: Saccharomycetes cerevisiae  
C:Date: 26-Aug-1994 #sequence\_revision 09-Sep-1994 #text\_change 19-Apr-2002  
C:Accession: S45900  
R:Andre, B.; Cziepluch, C.; Hein, C.; Jauniaux, J.C.; Urrestarazu, A.; Visser, S.  
Submitted to the Protein Sequence Database, August 1994  
A:Reference number: S45893  
A:Accession: S45900  
A:Molecule type: DNA  
A:Residues: 1-397 <AND>  
A:Cross-references: EMBL:Z35911; NID:G536265; PIDN:CAA84984.1; PID:G536266; GSPDB:GN00000  
A:Experimental source: strain S288C  
C:Genetics:  
A:Gene: MIPS:YBR042c  
A:Cross-references: SGD:S0000246  
A:Map position: 2R  
C:Superfamily: probable membrane protein YBR042c  
C:Keywords: transmembrane protein  
F:12-37/Domain: transmembrane #status predicted <TM1>  
F:55-77/Domain: transmembrane #status predicted <TM2>  
F:134-150/Domain: transmembrane #status predicted <TM3>  
F:372-390/Domain: transmembrane #status predicted <TM4>

Query Match 14.0%; Score 271; DB 2; Length 397;  
Best Local Similarity 24.6%; Pred. No. 9.2e-16;  
Matches 87; Conservative 72; Mismatches 122; Indels 72; Gaps 13;  
QY 8 VVVP-LGLLFFASGLLVNLIQAICYVVRPVSKSLY-----RRINRWVAELLWLELV-W 59  
Db 13 VVVPGLSLIIFQGCILILFLQLTY-----KTLYCRNDIRKQIGLNKTKRLFIVLVSS 65  
QY 60 LIDWAGVKVQIFTDHE-----TF-----RLMG--KEHALVISNHRSDIDWLVGWSA 105  
Db 66 ILHVVAFAVAVRITTESSVVPKGTFFDLKLRILSHLKSNSVAICNHQIYTDWIFLWLA 125  
QY 106 QRSGLGSTLAVMKKSKFPLPVIGWSMWFSEYLFERSWAKDESTLKSQI----- 155  
Db 126 YTSNLGANVFIILKKSLASIPILGFGWRNRYNFIEMSRKWAQDKITLSNSLAGLDSNARGA 185  
QY 156 -----QRLSD-----FPLPFWLALFVEGTRFTQAKLLAAQEAATSTG 192  
Db 186 GSLAGKSPERITEEGESWNPEVIDPKQIHWPNYLLIFPEGTNLSADTRQKSAKYAAKIG 245  
QY 193 LPVPRNVLPRTKGFVSASHMRSFVPAIYDVTVAIP--KSSPAPTMRLFLXG-----Q 244  
Db 246 KKFKNVLLPHSTGLRYSLOKLPKPSIESLYDITIGYSGVQKEEYGLIYGLKSLFLEGKY 305  
QY 245 PSVVHVIKRLHLMKELPDTE-VAQWCRDIFVAKDALLDKHMAEGTTF-SDQE 295  
Db 306 PKLVDIHIRAFDVKDIPLEDENEFSEWLYKIWSEKDALMERYYSTGTSFVSDPE 358

RESULT 10  
T34057  
hypothetical protein F28B3.5 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
C:Accession: T34057  
R:Geisel, C.; Kramer, J.; Smith, A.  
Submitted to the EMBL Data Library, May 1997  
A:Description: The sequence of C. elegans cosmid F28B3.  
A:Reference number: Z21469

A:Molecule type: DNA  
A;Residues: 1-918 <GEI>  
A;Cross-references: EMBL:AF003136; PIDN:AB93636.1; GSPDB:GN00019; CESP:F28B3.5  
A;Experimental source: strain Bristol N2; clone F28B3  
C;Genetics:  
A;Gene: CESP:F28B3.5  
A;Map position: 1  
A;Introns: 85/3; 129/3; 235/3; 418/2; 482/3; 532/3; 736/3; 829/3; 850/2

Query Match 13.9%; Score 269; DB 2; Length 918;  
Best Local Similarity 26.3%; Pred. No. 4.2e-15;  
Matches 88; Conservative 67; Mismatches 119; Indels 60; Gaps 11;

Qy 1 MAIAAAVVVPLGLLF-----FASGLLVNLIQAICYVVVRPVSKSL-----YRINRV 48  
Db 539 IAVDALRPIIPCSSLSSLMVFFASCAIV--IGGSWIVPRHVAQQLDNMLYKSYMLCLF 596  
Qy 49 VAEILLWLELVWLDWAGVKVQIF-TDHTETRLMGK-EHALVISNHRSDIDWLGVWSAQ 106  
Db 597 VFENL-----SGVEIYLHGTTNEEVVNTKGPENAVMISNHSQSNVDWIIPVMLAA 645  
Qy 107 RSGCLGSTLA---VMKSSKFLPVIGSMWFSEYLFLEERSWAKDESTLKSIGIQLSDPPL 163  
Db 646 RHGDQGNQAFRVMVKNSTHLPVPMFGWYIFQHGYYIVRRFGEFIGAPVLRQLKWLNESDP 705  
Qy 164 PFWLALFVEGTRFTQAK---LLAAQEYATSTGLPVPVRNVLPRTKGFYSAVSHMRSFVPA 220  
Db 706 PYWLLIFPEGTRNSAKKHULESSNRFLEKSGRQPMQNVLCPRSGGLQALDNL-SFLDA 764  
Qy 221 IYDVTV-----AIPKSSPAPTMLRLFKG--QPSVVHVHIKR 254  
Db 765 IYDVTVMYQMRFDLGLNLTIHYNLIIVYMAERRGLAPGMDFCCGSQQFKQLHIHLDR 824  
Qy 255 HLMKELPDTEAQAQWCRDIFVAKDALLDKHMAE 288  
Db 825 IPIDEVPKAKLELRTWTIERFTKKEIIDFYSE 858

RESULT 11  
T22689  
hypothetical protein F55A11.5 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C;Accession: T22689  
R;Kershaw, J.  
submitted to the EMBL Data Library, May 1996  
A;Reference number: Z19600  
A;Accession: T22689  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A;Residues: 1-439 <WIL>  
A;Cross-references: EMBL:Z72511; PIDN:CAA96659.1; GSPDB:GN00023; CESP:F55A11.5  
A;Experimental source: clone F55A11  
C;Genetics:  
A;Gene: CESP:F55A11.5  
A;Map position: 5  
A;Introns: 19/3; 52/2; 176/1; 222/3; 260/2; 327/1; 342/1

Query Match 12.9%; Score 250; DB 2; Length 439;  
Best Local Similarity 25.1%; Pred. No. 7.1e-14;  
Matches 65; Conservative 54; Mismatches 106; Indels 34; Gaps 4;

Qy 60 LIDWAGVKVQIFTDHTETRLMGKEHALVISNHRSDIDWLGVWSAQRSQ--CLGSTLAV 117  
Db 21 LLEFLMGVRIRVSGDEIEF-----GSPAMIVMNRTRLDWMVMWCALYQINPWLITSNKIS 76  
Qy 118 MKKSSKFLPVIGSMWFSEYLFLEERSWAKDESTLKSIGIQLSDPPLPFWLALFVEGTRFT 177  
Db 77 LKAQLKLLPGAGFGMAAAQVFLERNAEVDKRSFDDAIDYFKNIDKKYQILLFPEGTDKS 136  
Qy 178 QAKLLAAQEYATSTGLPVPVRNVLPRTKGFYSAVSHMR----- 215  
Db 137 EWTILKSREFAKKNGLRHLDVLYPRTTGTGFLHLNKMREPSSSVIRFKNVHFYFIKIQK 196

Qy 216 -----SFVPAIYDVTVAIPKSSPAPTMLRLFKG-QPSVVHVHIKRHLMKELPDTDEAVAQ 269  
Db 197 IILLEEYVEYIIDITAIYPYNIVQSEIDLVLKGASPREVHFHIRKIPISQVPLNEQDASR 256  
Qy 270 WCRDIFVAKDALLDKHMAE 288  
Db 257 WLTDRTWTIKEQLLHDFYSE 275

RESULT 12  
S54641  
probable membrane protein YDR018c - yeast (Saccharomyces cerevisiae)  
N;Alternate names: hypothetical protein D3246; hypothetical protein PZF396; hypothetical  
C;Species: Saccharomyces cerevisiae  
C;Date: 08-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 19-Apr-2002  
C;Accession: S54641; S63425; S67831; S72116  
R;Dedman, K.; Brown, D.; Hamlyn, N.; Bowman, S.  
submitted to the EMBL Data Library, May 1995  
A;Reference number: S54638  
A;Accession: S54641  
A:Molecule type: DNA  
A;Residues: 1-396 <DED>  
A;Cross-references: EMBL:Z49770; NID:G840867; PIDN:CAA89843.1; PID:G840871  
A;Experimental source: strain AB972  
R;Eide, L.G.; Sander, C.; Prydz, H.  
submitted to the EMBL Data Library, February 1996  
A;Description: Sequencing and analysis of a 35.4 kb region on the left arm of chromosome  
A;Reference number: S63416  
A;Accession: S63425  
A:Molecule type: DNA  
A;Residues: 1-396 <EID>  
A;Cross-references: EMBL:X95966; NID:G1216215; PIDN:CAA65210.1; PID:G1216225  
R;Prydz, H.; Eide, L.G.  
submitted to the Protein Sequence Database, July 1996  
A;Reference number: S67822  
A;Accession: S67831  
A:Molecule type: DNA  
A;Residues: 1-396 <PRY>  
A;Cross-references: EMBL:Z74314; NID:G1431443; PIDN:CAA98838.1; PID:G1431444; MIPS:YDR01  
A;Experimental source: strain S288C  
R;Eide, L.G.; Sander, C.; Prydz, H.  
Yeast 12, 1085-1090, 1996  
A;Title: Sequencing and analysis of a 35.4 kb region on the left arm of chromosome IV f  
A;Reference number: S72107; MUID:97051598; PMID:8896275  
A;Accession: S72116  
A;Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A;Residues: 1-396 <EIW>  
A;Cross-references: EMBL:X95966; NID:G1216215; PIDN:CAA65210.1; PID:G1216225  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996  
C;Genetics:  
A;Cross-references: SGD:S0002425  
A;Map position: 4R  
A;Note: YDR018C  
C;Superfamily: probable membrane protein YBR042c  
C;Keywords: transmembrane protein  
F;27-43/Domain: transmembrane #status predicted <TM1>  
F;69-85/Domain: transmembrane #status predicted <TM2>  
F;376-392/Domain: transmembrane #status predicted <TM3>

Query Match 12.8%; Score 247; DB 2; Length 396;  
Best Local Similarity 25.8%; Pred. No. 1.1e-13;  
Matches 85; Conservative 61; Mismatches 129; Indels 54; Gaps 11;

Qy 17 FASGLLVNLIQAICYVVVRPVSKSLYRR-INRVVAELLWLLELVWLDWAGVKVQIFTDH 75  
Db 33 FISGSLIVVFQICLVQLVLLPWSKIRFQNGINQSKAFIVL-LCMILNMVAPSSLNV--TF 89  
Qy 76 ETFRIMG-----KEHALVISNHRSDIDWLGVWSAQRSGLGSTLAVMKSSKF 124  
Db 90 ETSRPLKNSSNAKPCFRFKDRAIIIANHQMAYDIWLWLSFVSNLGNVVIILKALQY 149

```

125 LPVIGSNWFSEYLFILERSWAKDESTL-----KSGIQLRSLDFPLP 164
   : : : : : : : : : : : : : : : : : : : : : : : :
150 IPLLGFGRNFKFIPLSRNWQKDEKALTNLSVMDLNARCKGPLTNYKSCYKTNESIAA 209
   : : : : : : : : : : : : : : : : : : : : : : : :
165 FWLALFVEGTRF---TQAKLLAQEYATSTGLPVRNVLIPTKGFVSAYSHMRSFVDAI 221
   : : : : : : : : : : : : : : : : : : : : : : : :
210 YNLIMFPEGTNLSLKTRKSEAFQRAHLDHVOL-RHLLLEHSGKGLKFAVEKLAPSLDAI 268
   : : : : : : : : : : : : : : : : : : : : : : : :
222 YDVTVAIPKSSPAP-----TMLRLF--KGQPSVVHVHVKRHLMKELP-DTDEAVAQ 269
   : : : : : : : : : : : : : : : : : : : : : : : :
269 YDVTIGY---SPALRTEYVGTGKFIKILFMGVYPEKVDVFIREFRVNEIPLQDDEVEFN 325
   : : : : : : : : : : : : : : : : : : : : : : : :
270 WCRDIFVAKDALLDKHMAEGTFSDQELQD 298
   : : : : : : : : : : : : : : : : : : : : : : : :
326 WLLGWVKEKDQLLEDYNTGOFKSNAKND 354
   : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 13  
T25998  
hypothetical protein ZK40.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T25998  
R:Bradshaw, H.  
submitted to the EMBL Data Library, July 1996  
A:Description: The sequence of C. elegans cosmid ZK40.  
A:Reference number: Z20121  
A:Accession: T25998  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-523 <BRA>  
A:Cross-references: EMBL:U64839; PIDN:AAB04844.1; GSPDB:GN00023; CESP:ZK40.1  
A:Experimental source: strain Bristol N2; clone ZK40  
C:Genetics:  
A:Gene: CESP:ZK40.1  
A:Map position: 5  
A:Introns: 7/1; 38/3; 93/3; 126/3; 160/1; 301/3; 422/2; 472/3

RESULT 14  
B83541  
probable polynucleotide adenyllyltransferase (EC 2.7.7.19) II PA0834 [similarity] - Pseud  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 02-Mar-2001  
C;Accession: B83541

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: B83541  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-304 <STO>  
A:Cross-references: GB:AE004518; GB:AE004091; NID:g9946725; PIDN:AAG04223.1; GSPDB:GN001  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA0834  
C:Superfamily: Escherichia coli polynucleotide adenyltransferase II yihG  
C:Keywords: nucleotidyltransferase

Query Match	8.3%;	Score 160.5;	DB 2;	Length 304;
Best Local Similarity	23.6%;	Pred. No. 2.7e-06;		
Matches	74;	Conservative 50;	Mismatches 112;	Indels 77; Gaps 14;
Qy	13	GLLFFASGL-----LVNLI-----QAICYVVVRPVSKSLYRRINRVVAELLWLE	56	
Db	15	GLLLVSTLCWACLLPFGMTLVKLLLPFAAAQRLCSKIMSLIAEGW-----IACNKGWMN	68	
Qy	57	LV-----WLIDWAGVKVQIFTDHETFRLMGKEHA-LVINSNHRSDIDWLGVWVSAQRSGL	111	
Db	69	LVQRTRNVOGLELEYQ-----HSYLVTSNHQSVDILV--LQYQLNRRI	112	
Qy	112	GSTLAVMKSSKFLPVIGSMWFSEYLELER-----SWAKDESTLSGIIQRLSD	160	
Db	113	PLLRFFLQELIWPPIIGLCWWALDFPFMKRYSKAYLARHPEKKGQDLATRKACAKPSR	172	
Qy	161	FPLPFWLALFVEGTRFTQAKLLAAQEVATSTGLPVP--RVNLIIPRTKGFVSAVSHMRSFVP	219	
Db	173	IPVAVF--NFLEGRTRFRAKHDEQQS-----PPRHLKPKAGGIAFVLDAMGEQLK	221	
Qy	220	AIYDVTVAIPKSSPAPTMLRLFKGQPSVY-----HVHIKRLMKELPDTEA-----VAQW	270	
Db	222	TLVNVTIHPDGS--PFWCLLSGRLKDVVVRFEELI:PRQFVGKSYDQAGYRAEFQOW	279	
Qy	271	CRDIFVAKDALLD	283	
Db	280	VNQLWERKDQLLD	292	

RESULT 15  
S40808  
polynucleotide adenyllyltransferase (EC 2.7.7.19) II yihG [validated] - Escherichia coli  
C;Species: Escherichia coli  
C;Date: 19-May-1994 #sequence revision 01-Sep-1995 #text\_change 01-Mar-2002  
C;Accession: S40808; J06149; E065191  
R;Plunkett III, G.; Burland, V.; Daniels, D.L.; Blattner, F.R.  
Nucleic Acids Res. 21, 3391-3398, 1993  
A;Title: Analysis of the Escherichia coli genome. III. DNA sequence of the region from 8  
A;Reference number: S40802; MUID:93347969; PMID:8346018  
A;Accession: S40808  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-310 <PLU>  
A;Cross-references: EMBL:L19201; NID:G304961; PIDN:AAB02997.1; PID:G304968  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1993  
R;Cao, G.J.; Pogliano, J.; Sarkar, N.  
Proc. Natl. Acad. Sci. U.S.A. 93, 11580-11585, 1996  
A;Title: Identification of the coding region for a second poly(A) polymerase in Escherichia coli  
A;Reference number: J06149; MUID:97030237; PMID:8876178  
A;Accession: J06149  
A;Molecule type: DNA  
A;Residues: 1-310 <CAO>  
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A;Title: The complete genome sequence of Escherichia coli K-12



A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: B65191  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-310 <BLAT>  
A:Cross-references: GB:AE000461; GB:U00096; NID:G2367318; PIDN:AAC76860.1; PID:gl790293;  
A:Experimental source: strain K-12, substrain MGL655  
C:Genetics:  
A:Gene: yihG  
C:Superfamily: Escherichia coli polynucleotide adenyltransferase II yihG  
C:Keywords: nucleotidyltransferase

Query Match	7.6%	Score 148;	DB 2;	Length 310;
Best Local Similarity	21.6%	Fred. No. 3.4e-05;		
Matches	71;	Conservative 58;	Mismatches 115;	Indels 84; Gaps 14;

  

QY	6	AAVVVPLGLLFFASGLLVNLIQAICYV--VVRPVSKSL-----YRRINRWVAELLWLEL	57
Db	15	AAITLLLSI-----VLTILVTIFCSVPPIIAGIVKLLLPVPVIRKVSREFCFMVMYC--	66
QY	58	VWLIDWWAGVKVQIFTD-----HETFLMGKEHALVISNHRSDIDWLVGWVSAQRSGC	110
Db	67	-----WCEGLAVLLHLNPHLQWEVHGLEGLSKKNWYLLICNHRSWADIIVVLCVLFKXH--	119
QY	111	LGSTLAVMKKSKKFLPVIGSMWFSYLFLEL-----SWAKDESTLKSGIQRLS	159
Db	120	IPMKNKYFLKQQLAWVPFLGLACWSLDMPFMKRYSRAYLLRHPERRRGKDVETRRSCEK--	177
QY	160	DPPL-PFWLALFVEGTRFTQAKLLAAQEVATSTGLPVRNVLIPTKGFVS AVSHMRSFV	218
Db	178	-FRLHPTTIVNFVEGSRFTQEK--HQQTHSTF-----QNLPPKAAGIAMALNVLGKQF	228
QY	219	PAIYDVTVAIPKSSPAPTMLRFLFKGQPSVVVHVI-----KRHLMKKE	259
Db	229	DKLLNVTLCYDPNRRQP-FFDMLSGKLTIRIVVHVVDLQPIADELHGDIYNDKSFRRHFQ--	285
QY	260	LPDTDEAVAQWCRDIFVAKDALLDKDMA	287
Db	286	-----QWLSLWQEKDRLLTSLMS	304

Search completed: July 7, 2004, 13:41:49  
Job time : 22 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 7, 2004, 13:41:23 ; Search time 51 Seconds  
(without alignments)  
2301.059 Million cell updates/sec

Title: US-09-914-098-56  
Perfect score: 1935  
Sequence: 1 MAIAAAVVVPLGLFFASG.....QSRNPAKIVPAKSNKGS 377

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 1276540

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1935	100.0	377	12	US-10-424-599-278313 Sequence 278313,
2	1771	91.5	342	12	US-10-425-114-47952 Sequence 47952, A
3	1765.5	91.2	419	12	US-10-424-599-210085 Sequence 210085,
4	1731	89.5	406	12	US-10-425-114-57801 Sequence 57801, A
5	1695	87.6	399	12	US-10-425-114-51954 Sequence 51954, A
6	1592	82.3	319	12	US-10-424-599-278291 Sequence 278291,
7	1523	78.7	377	8	US-08-818-581B-4 Sequence 4, Appli
8	1459.5	75.4	425	12	US-10-425-114-67316 Sequence 67316, A
9	1451.5	75.0	419	12	US-10-425-114-66105 Sequence 66105, A
10	1450.5	75.0	374	9	US-09-970-989-5 Sequence 5, Appli
11	1450.5	75.0	374	12	US-10-667-494-5 Sequence 5, Appli
12	1450.5	75.0	374	16	US-10-667-462-5 Sequence 5, Appli
13	1450.5	75.0	374	16	US-10-667-464-5 Sequence 5, Appli
14	1442.5	74.5	375	8	US-08-818-581B-5 Sequence 5, Appli
15	1438.5	74.3	374	16	US-10-437-963-130474 Sequence 130474,

16	1301	67.2	380	12	US-10-425-114-49811	Sequence 49811, A
17	1156.5	59.8	311	8	US-08-818-581B-6	Sequence 6, Appli
18	999.5	51.7	263	12	US-10-425-114-70268	Sequence 70268, A
19	899.5	46.5	239	12	US-10-425-114-51896	Sequence 51896, A
20	856	44.2	266	12	US-10-425-114-56564	Sequence 56564, A
21	628	32.5	368	10	US-09-946-374-297	Sequence 297, App
22	628	32.5	368	12	US-10-206-915-338	Sequence 338, App
23	628	32.5	368	12	US-10-199-670-338	Sequence 338, App
24	628	32.5	368	12	US-10-201-858-338	Sequence 338, App
25	628	32.5	368	12	US-10-205-890-338	Sequence 338, App
26	628	32.5	368	12	US-10-208-024-338	Sequence 338, App
27	628	32.5	368	12	US-10-201-853-338	Sequence 338, App
28	628	32.5	368	12	US-10-174-581-338	Sequence 338, App
29	628	32.5	368	12	US-10-176-483-338	Sequence 338, App
30	628	32.5	368	12	US-10-176-749-338	Sequence 338, App
31	628	32.5	368	12	US-10-176-914-338	Sequence 338, App
32	628	32.5	368	12	US-10-176-915-338	Sequence 338, App
33	628	32.5	368	12	US-10-006-485A-297	Sequence 297, App
34	628	32.5	368	12	US-10-013-907A-297	Sequence 297, App
35	628	32.5	368	12	US-10-015-499A-297	Sequence 297, App
36	628	32.5	368	12	US-10-176-484-338	Sequence 338, App
37	628	32.5	368	12	US-10-180-550-338	Sequence 338, App
38	628	32.5	368	12	US-10-183-014-338	Sequence 338, App
39	628	32.5	368	12	US-10-187-738-338	Sequence 338, App
40	628	32.5	368	12	US-10-187-740-338	Sequence 338, App
41	628	32.5	368	12	US-10-187-883-338	Sequence 338, App
42	628	32.5	368	12	US-10-194-363-338	Sequence 338, App
43	628	32.5	368	12	US-10-194-460-338	Sequence 338, App
44	628	32.5	368	12	US-10-194-463-338	Sequence 338, App
45	628	32.5	368	12	US-10-194-484-338	Sequence 338, App

ALIGNMENTS

RESULT 1  
US-10-424-599-278313  
; Sequence 278313, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David X  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER-OF-SEQ ID NOS: 285684  
; SEQ ID NO 278313  
; LENGTH: 377  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_9333C.1.pep  
US-10-424-599-278313

Query Match	100.0%	Score	1935	DB	12	Length	377
Best Local Similarity	100.0%	Pred. No.	8.4e-195				
Matches	377	Conservative	0	Mismatches	0	Indels	0
						Gaps	0
QY	1	MAIAAAVVVPLGLLFFASGLLVNLIQAI	CVVVRPVSKSLYRRINRVVAELLWLELWVL	60			
Db	1	MAIAAAVVVPLGLLFFASGLLVNLIQAI	CVVVRPVSKSLYRRINRVVAELLWLELWVL	60			
QY	61	IDWWAGVKVQIFTDTHETFRMGKEHALVISNHRSDIDWL	VGWVSAQRSGCLGSLTAVMKK	120			
Db	61	IDWWAGVKVQIFTDTHETFRMGKEHALVISNHRSDIDWL	VGWVSAQRSGCLGSLTAVMKK	120			
QY	121	SSKFLPVIWGSWMWFSEYLFELERSWAKDESLKSGIQ	LSDFPLPFWLALFVEGTRTQAK	180			
Db	121	SSKFLPVIWGSWMWFSEYLFELERSWAKDESLKSGIQ	LSDFPLPFWLALFVEGTRTQAK	180			

QY 181 LLAQBYATSTGLPVPRNVLIPTKGFVSASHMRSFVPAIYDVTVAIPKSSPAPTMRL 240  
DB 181 LLAQBYATSTGLPVPRNVLIPTKGFVSASHMRSFVPAIYDVTVAIPKSSPAPTMRL 240  
QY 241 FKQPSVHVHVKRHLMKELPOTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQELQDTG 300  
DB 241 FKQPSVHVHVKRHLMKELPOTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQELQDTG 300  
QY 301 RPIKSLVWISWACLVVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMQILIQFSQSE 360  
DB 301 RPIKSLVWISWACLVVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMQILIQFSQSE 360  
QY 361 RSNPAKIVPAKSKNKG 377  
DB 361 RSNPAKIVPAKSKNKG 377

## RESULT 2

US-10-425-114-47952  
; Sequence 47952, Application US/10425114  
; Publication No. US20040034888A1

## GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 47952

; LENGTH: 342

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: 700909008\_FLI.pep

US-10-425-114-47952

Query Match 91.5%; Score 1771; DB 12; Length 342;  
Best Local Similarity 100.0%; Pred. No. 1.4e-177;  
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 PVSKSLYRRINRVVAELLWLELVWLDWAGVKVQIFDTHETFRMGKEHALVISNHRSD 95  
DB 1 PVSKSLYRRINRVVAELLWLELVWLDWAGVKVQIFDTHETFRMGKEHALVISNHRSD 60  
QY 96 IDWLGVWVSAQRSGCLGSTLAVMKSKKFLPVIGSMWFSEYLFLEERSWAKDESTLXSGI 155  
DB 61 IDWLGVWVSAQRSGCLGSTLAVMKSKKFLPVIGSMWFSEYLFLEERSWAKDESTLXSGI 120  
QY 156 QRLSDPFLPFWLALFVEGTRFTQAKLLAAQBYATSTGLPVPRNVLIPTKGFVSASHMR 215  
DB 121 QRLSDPFLPFWLALFVEGTRFTQAKLLAAQBYATSTGLPVPRNVLIPTKGFVSASHMR 180  
QY 216 SFVPAIYDVTVAIPKSSPAPTMRLFKGQPSVHVHVKRHLMKELPOTDEAVAQWCRDIF 275  
DB 181 SFVPAIYDVTVAIPKSSPAPTMRLFKGQPSVHVHVKRHLMKELPOTDEAVAQWCRDIF 240  
QY 276 VAKDALLDKHMAEGTFSQELQDTGRPIKSLVWISWACLVVAGSVKFLQWSSLLSSWKG 335  
DB 241 VAKDALLDKHMAEGTFSQELQDTGRPIKSLVWISWACLVVAGSVKFLQWSSLLSSWKG 300  
QY 336 VAFSAFGLAVVTALMQILIQFSQERSNPAPKIVPAKSKNKG 377  
DB 301 VAFSAFGLAVVTALMQILIQFSQERSNPAPKIVPAKSKNKG 342

## RESULT 3

US-10-424-599-210085  
; Sequence 210085, Application US/10424599  
; Publication No. US20040031072A1

## GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 210085

; LENGTH: 419

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_31735C.1.pap

US-10-424-599-210085

Query Match 91.2%; Score 1765.5; DB 12; Length 419;  
Best Local Similarity 91.9%; Pred. No. 7.1e-177;  
Matches 340; Conservative 12; Mismatches 17; Indels 1; Gaps 1;

QY 6 AAVVPLGLLFFASGLVNLQAIQCYVVRPVSKSLYRRINRVVAELLWLELVWLDWMA 65  
DB 38 SAVVPLGLLFFASGLVNLQAIQCYVVRPVSKSLYRRINRVVAELLWLELVWLDWMA 97  
QY 66 GVKVQIFDTHETFRMGKEHALVISNHRSDIDWLGVWVSAQRSGCLGSTLAVMKSKKFL 125  
DB 98 GVKVQIFDTHETFRMGKEHALVISNHRSDIDWLGVWVSAQRSGCLGSTLAVMKSKKFL 157  
QY 126 PVIGSMWFSEYLFLEERSWAKDESTLXSGIQRLSDPFLPFWLALFVEGTRFTQAKLLAAQ 185  
DB 158 PVIGSMWFSEYLFLEERSWAKDESTLXSGIQRLSDPFLPFWLALFVEGTRFTQAKLLAAQ 217  
QY 186 EYATSTGLPVPRNVLIPTKGFVSASHMRSFVPAIYDVTVAIPKSSPAPTMRLFKGQP 245  
DB 218 EYASAGLPVPRNVLIPTKGFVSASHMRSFVPAIYDVTVAIPKSSPAPTMRLFKGQP 277  
QY 246 SVVHVHVKRHLMKELPOTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQELQDTGRPIKS 305  
DB 278 SVVHVHVKRHLMKELPOTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQELQDTGRPIKS 337  
QY 306 LLVWISWACLVVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMQILIQFSQERSNPA 365  
DB 338 LLVWISWACLVVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMQILIQFSQERSNPA 397  
QY 366 KIVPA-KSKN 374  
DB 398 KVAPTKSKN 407

## RESULT 4

US-10-425-114-57801

; Sequence 57801, Application US/10425114

; Publication No. US20040034888A1

## GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 57801

```

; LENGTH: 406
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701127504_FLI.pap
US-10-425-114-57801

Query Match      89.5%; Score 1731; DB 12; Length 406;
Best Local Similarity 89.4%; Pred. No. 2.9e-173;
Matches 330; Conservative 17; Mismatches 22; Indels 0; Gaps 0;

Qy 6 AAVVPLGLLFFASGLLVNLIQAICVYVVRPVSKSLYRRINRVVAELLWLWLDWA 65
Db 26 AVVVPLGLLFFASGLLVNLIQAICVYVVRPVSKNLYRRMNRVVAELLWLWLDWA 85

Qy 66 GVKVQIETDTHETFLRMGKEHALVISNHRSDIDLWLVGVSAQRSGLGSTLAVMKSSKFL 125
Db 86 GVKVQVETDPTETFRSMGKEHALVISNHRSDIDLWLVGVLAQRSGLGSTLAVMKSSKFL 145

Qy 126 PVIGSMWFSEYLFLEERSWAKDESTLKSGIQRLSDFFLPFWLALFVEGTRFTQAKLLAAQ 185
Db 146 PVIGSMWFSEYLFLEERSWAKDERTLKSGLQQLRDFFLPFWLALFVEGTRFTQAKLLAAQ 205

Qy 186 EYATSTGLPVPRNVLIPTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMRLFRGKS 245
Db 206 EYAASAGLPVPRNVLIPTKGFVSAVNHMRSFVPAIYDVTVAIPKSSPAPTMRLFRGKS 265

Qy 246 SVHVHVKRHKMLKELPDTDEAVAQWCRDIFVAKDALLDKMAEGTFSDOELQDTGRPIKS 305
Db 266 SVHVHVKRHKMKDLPEDEAVAQWCRDMFVAKDTLLDKHIAEDTFSDOELQDTGRPIKS 325

Qy 306 LLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMQILIQFSQSERSNPA 365
Db 326 LVVVISWACVVVMGVKFLQWSSLLSSWKGVAFAFGLGVVTVLLMHILIMFSQSERSPT 385

Qy 366 KIVPAKSKN 374
Db 386 KVAPAKSKN 394

RESULT 5
US-10-425-114-51954
; Sequence 51954, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 51954
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700844230_FLI.pap
US-10-425-114-51954

Query Match      87.6%; Score 1695; DB 12; Length 399;
Best Local Similarity 87.8%; Pred. No. 1.8e-169;
Matches 325; Conservative 20; Mismatches 23; Indels 2; Gaps 2;

Qy 6 AAVVPLGLLFFASGLLVNLIQAICVYVVRPVSKSLYRRINRVVAELLWLWLDWA 65
Db 19 AVVVPLGLLFFASGLLVNLIQAICVYVVRPVSKNLYRRMNRVVAELLWLWLDWA 78
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Qy 66 GVKVQIETDTHETFLRMGKEHALVISNHRSDIDLWLVGVSAQRSGLGSTLAVMKSSKFL 125
Db 79 GVKVQVETDPTETFRSMGKEHALVISNHRSDIDLWLVGVLAQRSGLGSTLAVMKSSKFL 137

Qy 126 PVIGSMWFSEYLFLEERSWAKDESTLKSGIQRLSDFFLPFWLALFVEGTRFTQAKLLAAQ 185
Db 138 PVIGSMWFSEYLFLEERSWAKDERTLKSGLQQLRDFFLPFWLALFVEGTRFTQAKLLAAQ 197

Qy 186 EYATSTGLPVPRNVLIPTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMRLFRGKS 245
Db 198 EYAASAGLPVPRNVLIPTKGFVSAVNHMRSFVPAIYDVTVAIPKSSPAPTMRLFRGKS 257

Qy 246 SVHVHVKRHKMLKELPDTDEAVAQWCRDIFVAKDALLDKMAEGTFSDOELQDTGRPIKS 305
Db 258 SLVHVHVKRHKMKDLPEDEAVAQWCRDVFVAKDALLDKMAEDTFSDOELQDTGRPVKS 317

Qy 306 LLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMQILIQFSQSERSNPA 365
Db 318 LVVVISWACVVVMGVKFLQWSSLLSSWKGVAFAFGLGVVTVLLMHILIMFSQSERSPTS 377

Qy 366 KIVPA-KSKN 374
Db 378 KVAPTCKSKN 387

RESULT 6
US-10-424-599-278291
; Sequence 278291, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 278291
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(319)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_9331C.1.pap
US-10-424-599-278291

Query Match      82.3%; Score 1592; DB 12; Length 319;
Best Local Similarity 84.4%; Pred. No. 9.2e-159;
Matches 318; Conservative 0; Mismatches 1; Indels 58; Gaps 1;

Qy 1 MAIAAAVAVVPLGLLFFASGLLVNLIQAICVYVVRPVSKSLYRRINRVVAELLWLW 60
Db 1 MAIAAAVAVVPLGLLFFASGLLVNLIQAICVYVVRPVSKSLYRRINRVVAELLWLW 60

Qy 61 IDWWAGVKVQIETDTHETFLRMGKEHALVISNHRSDIDLWLVGVSAQRSGLGSTLAVMK 120
Db 61 IDWWAGVKVQIETDTHETFLRMGKEHALVISNHRSDIDLWLVGVSAQRSGLGSTLAVMK 120

Qy 121 SSKFLPVIGSMWFSEYLFLEERSWAKDESTLKSGIQRLSDFFLPFWLALFVEGTRFTQAK 180
Db 121 SSKFLPVIGSMWFSEYLFLEERSWAKDESTLKSGIQRLSDFFLPFWLALFVEGTRFTQAK 180

Qy 181 LLAAQYATSTGLPVPRNVLIPTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMRL 240
Db 181 LLAAQYATSTGLPVPRNVLIPTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMRL 240

Qy 241 FKGPQSVVHVHVKRHKMLKELPDTDEAVAQWCRDIFVAKDALLDKMAEGTFSDOELQDTG 300
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Db 241 FRGQPSVHVH-----251  
QY 301 RPIKSLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE 360  
Db 252 -----IXWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE 302  
QY 361 RSNPAKIVPAKSKNKG 377  
Db 303 RSNPAKIVPAKSKNKG 319

RESULT 7  
US-08-818-581B-4  
; Sequence 4, Application US/08818581B  
; Publication No. US20020007499A1  
; GENERAL INFORMATION:  
; APPLICANT: SLABAS, Antoni Ryszard  
; APPLICANT: BROWN, Adrian Paul  
; APPLICANT: BROUGH, Clare Louise  
; APPLICANT: KROON, Johannes Theodorus Maria  
; TITLE OF INVENTION: DNA SEQUENCE ENCODING PLANT  
; TITLE OF INVENTION: 2-ACYLTRANSFERASE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: US  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/818,581B  
; FILING DATE: March 14, 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/GB96/00306  
; FILING DATE: 09-FEB-1996  
; APPLICATION NUMBER: GB 9502468.3  
; FILING DATE: 09-FEB-1995  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 377 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-818-581B-4

Query Match 78.7%; Score 1523; DB 8; Length 377;  
Best Local Similarity 77.3%; Pred. No. 2.2e-151;  
Matches 283; Conservative 43; Mismatches 40; Indels 0; Gaps 0;  
QY 1 MAIAAAAVVPLGLLFFASGLLVNLIQAICYVVVRPVSKSLYRINRVVAELLMLELVWL 60  
Db 1 MAIAAAAFIVPISLLFFMSGLVNVNFIQAVFYVLRVPISKOTYRRINTLVAEELLMLELVW 60  
QY 61 IDWAGVKVQIFTDHETFRMLGKHEHALVISNHRSDIDWLVGVSAQSGCLGSTLAVMKK 120  
Db 61 IDWAGVKVQLYDDETFRMLGKHEHALVISNHRSDIDWLVGVSAQSGCLGSTLAVMKK 120  
QY 121 SSKFLPVIGWSMWFSEYLFRLSWAKDESTLKSIGIQRSLDPLPFWLALFVEGTRFTQAK 180  
Db 121 SSKFLPVIGWSMWFSEYLFRLSWAKDESTLKSIGIQRSLDPLPFWLALFVEGTRFTQAK 180  
QY 181 LLAQAEYATSTGLPVPRNVLIPTKGFVSVMHRSFVPAIYDVTVVAIPKSSPAPTMLRL 240  
Db 181 LLAQAEYAAAGLIPVPRNVLIPTKGFVSVMHRSFVPAIYDLTVVAIPKTEQPTMLRL 240  
QY 241 FRGQPSVHVHVKRHLMKELPDDEAVAQWCEDIFVAKDALLDKHMAEGTFSQDELQDTG 300

Db 241 FRGKSSVVHVHVKRHLMKDLPKTDGVAQWCKDQFISKDALLDKHVAEDTFSGLEVDIG 300  
QY 301 RPIKSLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE 360  
Db 301 RPKSLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIRSSQSE 360  
QY 361 RSNPAK 366  
Db 361 HSTPAK 366

RESULT 8  
US-10-425-114-67316  
; Sequence 67316, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 67316  
; LENGTH: 425  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB4765-008-H3\_FLI.pep  
US-10-425-114-67316

Query Match 75.4%; Score 1459.5; DB 12; Length 425;  
Best Local Similarity 71.7%; Pred. No. 1.3e-144;  
Matches 269; Conservative 48; Mismatches 57; Indels 1; Gaps 1;  
QY 1 MAIAAAAVVPLGLLFFASGLLVNLIQAICYVVVRPVSKSLYRINRVVAELLMLELVWL 60  
Db 52 MAIPLVLVPLGLLFLLSGLIVNTIQAIFVTIRPFPSKSLYRINRFLAEELMWLVVW 111  
QY 61 IDWAGVKVQIFTDHETFRMLGKHEHALVISNHRSDIDWLVGVSAQSGCLGSTLAVMKK 120  
Db 112 VDWAGVKVQLHADEETYSRSMGHEHALVISNHRSDIDWLVGILAQSGCLGSTLAVMKK 171  
QY 121 SSKFLPVIGWSMWFSEYLFRLSWAKDESTLKSIGIQRSLDPLPFWLALFVEGTRFTQAK 180  
Db 172 SSKFLPVIGWSMWFSEYLFRLSWAKDESTLKSIGIQRSLDPLPFWLALFVEGTRFTQAK 231  
QY 181 LLAQAEYATSTGLPVPRNVLIPTKGFVSVMHRSFVPAIYDVTVVAIPKSSPAPTMLRL 240  
Db 232 LLAQAEYAAASQGLPAPRNVLIPTKGFVSVMHRSFVPAIYDTTVIVPKDSPQPTMLRI 291  
QY 241 FRGQPSVHVHVKRHLMKELPDDEAVAQWCEDIFVAKDALLDKHMAEGTFSQDELQDTG 300  
Db 292 LKGQSSVHVHVRMKRHAMSEMPKSDDDVSKWCKDIFVAKDALLDKHLATGTF-DEEIRPIG 350  
QY 301 RPIKSLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE 360  
Db 351 RPKSLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIRSSQSE 410  
QY 361 RSNPAKIVPAKSKNKG 375  
Db 411 RSSAKAARNRVKKE 425

RESULT 9  
US-10-425-114-66105  
; Sequence 66105, Application US/10425114



Publication No. US20040034888A1  
GENERAL INFORMATION:  
APPLICANT: Liu, Jingdong  
APPLICANT: Zhou, Yihua  
APPLICANT: Kovalic, David K.  
APPLICANT: Screen, Steven E  
APPLICANT: Tabaska, Jack E  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53313)B  
CURRENT APPLICATION NUMBER: US/10/425,114  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 73128  
SEQ ID NO 66105  
LENGTH: 419  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: LIB4315-045-D9\_FLI.pep  
US-10-425-114-66105

Query Match 75.0%; Score 1451.5; DB 12; Length 419;  
Best Local Similarity 70.9%; Pred. No. 8.7e-144;  
Matches 266; Conservative 50; Mismatches 58; Indels 1; Gaps 1;

QY 1 MAIAAAAVVPLGLLFFASGLLVNLIQAICYVVRPVSKSLYRRINRVVAELLWLELVWL 60  
Db 46 MAIPLVVLPLGLLFFASGLLVNLIQAICYVVRPVSKSLYRRINRVVAELLWLELVWL 105  
QY 61 IDWWAGVKVQIFTDHETFRMGKEHALVISNHRSDIDWLVGWVSAQSGCLGSLTAVMKK 120  
Db 106 VDWWAGVKVQLHADEETYSRGMKEHALVISNHRSDIDWLVGWVSAQSGCLGSLTAVMKK 165  
QY 121 SSKFLPVIGSMWFESEYLFELERSWAKDESTLKSIGIQRISDFPLPFWLALFVEGTRFTQAK 180  
Db 166 SSKFLPVIGSMWFAEYLFELERSWAKDEKTLKWGLQRLKDFPRPFWLALFVEGTRFTPAK 225  
QY 181 LLAAQEVATSTGLPVPRNVLIPTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMRL 240  
Db 226 LLAAQEYAAASQGLPAPRNVLIPTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMRL 285  
QY 241 FKQPSVVVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQELQDTG 300  
Db 286 LKGQSSVIHVRMKRHAMSEMPKSDDDVSKWCKDIFVTKDALLDKHLATGTF-DEEIRPIG 344  
QY 301 RPIKSLVVISWACLWVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE 360  
Db 345 RPVKSLVTLFWSCLLLFGAIEFFKWTQLLSTWRGVAFTAAGMALVTGVMHVFMFSQAE 404  
QY 361 RSNPAKIVPAKSKNK 375  
Db 405 RSSAKAARNRVKKE 419

RESULT 10  
US-09-970-989-5  
Sequence 5, Application US/09970989  
Patent No. US20020156262A1  
GENERAL INFORMATION:  
APPLICANT: LEUNG, David W.  
APPLICANT: ADOUREL, Daniel  
APPLICANT: HOLLENBACK, David  
TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE  
FILE REFERENCE: 077319/0151  
CURRENT APPLICATION NUMBER: US/09/970,989  
CURRENT FILING DATE: 2001-10-05  
PRIOR APPLICATION NUMBER: 09/215,252  
PRIOR FILING DATE: 1998-12-18  
PRIOR APPLICATION NUMBER: US 08/618,651  
PRIOR FILING DATE: 1996-03-19  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 5  
LENGTH: 374  
TYPE: PRT  
ORGANISM: Maize  
US-09-970-989-5

Query Match 75.0%; Score 1450.5; DB 9; Length 374;  
Best Local Similarity 70.7%; Pred. No. 9.4e-144;  
Matches 265; Conservative 51; Mismatches 58; Indels 1; Gaps 1;

QY 1 MAIAAAAVVPLGLLFFASGLLVNLIQAICYVVRPVSKSLYRRINRVVAELLWLELVWL 60  
Db 1 MAIPLVVLPLGLLFFASGLLVNLIQAICYVVRPVSKSLYRRINRVVAELLWLELVWL 60  
QY 61 IDWWAGVKVQIFTDHETFRMGKEHALVISNHRSDIDWLVGWVSAQSGCLGSLTAVMKK 120  
Db 61 VDWWAGVKVQLHADEETYSRGMKEHALVISNHRSDIDWLVGWVSAQSGCLGSLTAVMKK 120  
QY 121 SSKFLPVIGSMWFESEYLFELERSWAKDESTLKSIGIQRISDFPLPFWLALFVEGTRFTQAK 180  
Db 121 SSKFLPVIGSMWFAEYLFELERSWAKDEKTLKWGLQRLKDFPRPFWLALFVEGTRFTPAK 180  
QY 181 LLAAQEVATSTGLPVPRNVLIPTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMRL 240  
Db 181 LLAAQEYAAASQGLPAPRNVLIPTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMRL 240  
QY 241 FKQPSVVVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQELQDTG 300  
Db 241 LKGQSSVIHVRMKRHAMSEMPKSDDESVKWKDIFVAKDALLDKHLATGTF-DEEIRPIG 299  
QY 301 RPIKSLVVISWACLWVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE 360  
Db 300 RPVKSLVTLFWSCLLLFGAIEFFKWTQLLSTWRGVAFTAAGMALVTGVMHVFMFSQAE 359  
QY 361 RSNPAKIVPAKSKNK 375  
Db 360 RSSAKAARNRVKKE 374

RESULT 11  
US-10-667-494-5  
Sequence 5, Application US/10667494  
Publication No. US20040043465A1  
GENERAL INFORMATION:  
APPLICANT: LEUNG, DAVID W.  
APPLICANT: ADOUREL, DANIEL  
APPLICANT: HOLLENBACK, DAVID  
TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE  
FILE REFERENCE: 077319/0275  
CURRENT APPLICATION NUMBER: US/10/667,494  
CURRENT FILING DATE: 2003-09-23  
PRIOR APPLICATION NUMBER: US/09/970,989A  
PRIOR FILING DATE: 2001-10-05  
PRIOR APPLICATION NUMBER: 09/215,252  
PRIOR FILING DATE: 1998-12-18  
PRIOR APPLICATION NUMBER: 08/618,651  
PRIOR FILING DATE: 1996-03-19  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 374  
TYPE: PRT  
ORGANISM: Zea mays  
US-10-667-494-5

Query Match 75.0%; Score 1450.5; DB 12; Length 374;  
Best Local Similarity 70.7%; Pred. No. 9.4e-144;  
Matches 265; Conservative 51; Mismatches 58; Indels 1; Gaps 1;

QY 1 MAIAAAAVVPLGLLFFASGLLVNLIQAICYVVRPVSKSLYRRINRVVAELLWLELVWL 60  
Db 1 MAIPLVVLPLGLLFFASGLLVNLIQAICYVVRPVSKSLYRRINRVVAELLWLELVWL 60



Publication No. US20020007499A1  
GENERAL INFORMATION:  
APPLICANT: SLABAS, Antoni Ryszard  
APPLICANT: BROWN, Adrian Paul  
APPLICANT: BROUGH, Clare Louise  
APPLICANT: KROON, Johannes Theodorus Maria  
TITLE OF INVENTION: DNA SEQUENCE ENCODING PLANT  
TITLE OF INVENTION: 2-ACYLTRANSFERASE  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: US  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/818,581B  
FILING DATE: March 14, 1997  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/GB96/00306  
FILING DATE: 09-FEB-1996  
APPLICATION NUMBER: GB 9502468.3  
FILING DATE: 09-FEB-1995  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 375 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Zea mays

US-08-818-581B-5

Query Match 74.5%; Score 1442.5; DB 8; Length 375;  
Best Local Similarity 70.4%; Pred. No. 6.6e-143;  
Matches 264; Conservative 51; Mismatches 59; Indels 1; Gaps 1;  
QY 1 MAIAAAAVVPLGLFFASGLLVNLIQAICYVVVRPVSKSLYRINRVVAELLMLELWVL 60  
Db 1 MAIPLVLVPLGLLFLLSGLIINAIAQVLFVIRPFKSFRRINRFLAELLMLELWVL 60  
QY 61 IDWAGVKVQIFTDHETFRMLGKEHALVISNHRSDIDWLVGVWSAQRSGCLGSLTAVMKK 120  
Db 61 VDWAGVKVQLHADEETYSRSMGLHALIISNHRSDIDWLVGWLIAQRSGCLGSLTAVMKK 120  
QY 121 SSKFLPVIGWSMWFSEYLFLEERSWAKDESTLKSIGIQRSLSDFFLFFWLALFVEGTRFTQAK 180  
Db 121 SSKFLPVIGWSMWFSEYLFLEERSWAKDESTLKSIGIQRSLSDFFLFFWLALFVEGTRFTQAK 180  
QY 181 LLAQEQYATSTGLPVPRNVLIPTKGFVSASVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240  
Db 181 LLAQEQYAAASQGLPAPRNVLIPTKGFVSASVIMRDFVPAIYDVTVIIPKDSQPQTMRLI 240  
QY 241 FKQPSVHVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQDELQDTG 300  
Db 241 LKGQSSVHVHVRKRAMSEMPKSEDDVSKWCKDIFVAKDALLDKHLATGTF-DEEIRPIG 299  
QY 301 RPIKSLLVVISWACLWVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE 360  
Db 300 RPKVKSLLVTLFWSCULLFQAEFFKWTQLLSTWGRGVAFTAGNALVTGMVHVFIMFSQAE 359  
QY 361 RSNPAKIVPAKSKNK 375  
Db 360 RSSSARAARNRVKKE 374

RESULT 15  
US-10-437-963-130474  
Sequence 130474, Application US/10437963  
Publication No. US20040123343A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
APPLICANT: Wu, Wei  
APPLICANT: Boukharov, Andrey A.  
APPLICANT: Barbazuk, Brad  
APPLICANT: Li, Ping  
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53221)B  
CURRENT APPLICATION NUMBER: US/10/437,963  
CURRENT FILING DATE: 2003-05-14  
NUMBER OF SEQ ID NOS: 204966  
SEQ ID NO 130474  
LENGTH: 374  
TYPE: PRT  
ORGANISM: Oryza sativa  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT4530\_32632C.1.pep  
US-10-437-963-130474

Query Match 74.3%; Score 1438.5; DB 16; Length 374;  
Best Local Similarity 72.1%; Pred. No. 1.7e-142;  
Matches 264; Conservative 46; Mismatches 55; Indels 1; Gaps 1;  
QY 1 MAIAAAAVVPLGLFFASGLLVNLIQAICYVVVRPVSKSLYRINRVVAELLMLELWVL 60  
Db 1 MAVPLVLVPLGLLFLLSGLIINAIAQVLFSLRPFKSLYRINRFLAELLMLELWVL 60  
QY 61 IDWAGVKVQIFTDHETFRMLGKEHALVISNHRSDIDWLVGVWSAQRSGCLGSLTAVMKK 120  
Db 61 VDWAGVKIQLHADEETYKAMGNEHALVISNHRSDIDWLVGWLIAQRSGCLGSLTAVMKK 120  
QY 121 SSKFLPVIGWSMWFSEYLFLEERSWAKDESTLKSIGIQRSLSDFFLFFWLALFVEGTRFTQAK 180  
Db 121 SSKFLPVIGWSMWFSEYLFLEERSWAKDESTLKSIGIQRSLSDFFLFFWLALFVEGTRFTQAK 180  
QY 181 LLAQEQYATSTGLPVPRNVLIPTKGFVSASVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240  
Db 181 LLAQEQYAVSQGLPAPRNVLIPTKGFVSATVIMRDFVPAIYDVTVIIPKDSQPQTMRLI 240  
QY 241 FKQPSVHVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQDELQDTG 300  
Db 241 LKGQSSVHVHVRKRAMSEMPKSEDDVSKWCKDIFVAKDALLDKHLATGTF-DEEIRPIG 299  
QY 301 RPIKSLLVVISWACLWVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE 360  
Db 300 RPKVKSLLVTLFWSCULLYGAVKLFLWTQLLSTWKGVGFTGLGLALVTAVMHVFIMFSQSE 359  
QY 361 RSNPAK 366  
Db 360 RSSSAK 365

Search completed: July 7, 2004, 13:47:18  
Job time : 52 secs



OM protein - protein search, using sw model

Run on: July 7, 2004, 13:38:43 ; Search time 23 Seconds  
(without alignments)  
846.217 Million cell updates/sec

Title: US-09-914-098-56  
Perfect score: 1935  
Sequence: 1 MAIAAAAVVPLGLLFFASG.....QSERSNPAKIVPAKSKNKGK 377

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score		Query Match		DB ID	Description
1	1523	78.7	377	4	US-08-818-581B-4	Sequence 4, Appli
2	1450.5	75.0	374	2	US-08-454-267-2	Sequence 2, Appli
3	1450.5	75.0	374	2	US-08-454-267-6	Sequence 6, Appli
4	1450.5	75.0	374	2	US-08-941-319-2	Sequence 2, Appli
5	1450.5	75.0	374	2	US-08-941-319-6	Sequence 6, Appli
6	1450.5	75.0	374	3	US-09-035-098-2	Sequence 2, Appli
7	1450.5	75.0	374	3	US-09-035-098-6	Sequence 6, Appli
8	1450.5	75.0	374	4	US-09-215-252-5	Sequence 5, Appli
9	1450.5	75.0	374	4	US-09-970-989A-5	Sequence 5, Appli
10	1442.5	74.5	375	4	US-08-818-581B-5	Sequence 5, Appli
11	1156.5	59.8	295	2	US-08-454-267-7	Sequence 7, Appli
12	1156.5	59.8	295	2	US-08-941-319-7	Sequence 7, Appli
13	1156.5	59.8	295	3	US-09-035-098-7	Sequence 7, Appli
14	1156.5	59.8	311	4	US-08-818-581B-6	Sequence 6, Appli
15	628	32.5	376	4	US-09-215-252-13	Sequence 13, Appli
16	628	32.5	376	4	US-09-970-989A-13	Sequence 13, Appli
17	554.5	28.7	378	4	US-09-215-252-17	Sequence 17, Appli
18	554.5	28.7	378	4	US-09-970-989A-17	Sequence 17, Appli
19	519.5	26.8	314	4	US-09-215-252-15	Sequence 15, Appli
20	519.5	26.8	314	4	US-09-970-989A-15	Sequence 15, Appli
21	304	15.7	353	2	US-08-996-306-4	Sequence 4, Appli
22	304	15.7	353	3	US-09-338-907-4	Sequence 4, Appli
23	304	15.7	353	4	US-09-218-207-4	Sequence 4, Appli
24	304	15.7	364	2	US-08-996-306-5	Sequence 5, Appli
25	304	15.7	364	3	US-09-338-907-5	Sequence 5, Appli
26	304	15.7	364	4	US-09-218-207-5	Sequence 5, Appli
27	303	15.7	354	3	US-09-338-907-74	Sequence 74, Appli

28	303	15.7	354	4	US-09-218-207-74	Sequence 74, Appli
29	242.5	12.5	228	3	US-09-338-907-70	Sequence 70, Appli
30	242.5	12.5	228	4	US-09-218-207-70	Sequence 70, Appli
31	219	11.3	315	3	US-09-338-907-134	Sequence 134, App
32	219	11.3	315	4	US-09-218-207-134	Sequence 134, App
33	211.5	10.9	291	3	US-09-338-907-127	Sequence 127, App
34	211.5	10.9	291	4	US-09-218-207-127	Sequence 127, App
35	210.5	10.9	300	3	US-09-338-907-135	Sequence 135, App
36	210.5	10.9	300	4	US-09-218-207-135	Sequence 135, App
37	187.5	9.7	261	3	US-09-338-907-128	Sequence 128, App
38	187.5	9.7	261	4	US-09-218-207-128	Sequence 128, App
39	174.5	9.0	185	3	US-09-338-907-136	Sequence 136, App
40	174.5	9.0	185	4	US-09-218-207-136	Sequence 136, App
41	160.5	8.3	346	4	US-09-252-991A-29402	Sequence 29402, A
42	157.5	8.1	319	4	US-09-540-236-3826	Sequence 3826, Ap
43	130.5	6.7	321	4	US-09-328-352-5730	Sequence 5730, Ap
44	130.5	6.7	364	4	US-09-252-991A-22552	Sequence 22552, A
45	129	6.7	182	3	US-09-338-907-133	Sequence 133, App

ALIGNMENTS

RESULT 1  
US-08-818-581B-4  
; Sequence 4, Application US/08818581B  
; Patent No. 6583340  
; GENERAL INFORMATION:  
; APPLICANT: SLABAS, Antoni Ryszard  
; APPLICANT: BROWN, Adrian Paul  
; APPLICANT: BROOK, Clare Louise  
; APPLICANT: KROON, Johannes Theodorus Maria  
; TITLE OF INVENTION: DNA SEQUENCE ENCODING PLANT  
; TITLE OF INVENTION: 2-ACYLTRANSFERASE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: US  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/818,581B  
; FILING DATE: March 14, 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/GB96/00306  
; FILING DATE: 09-FEB-1996  
; APPLICATION NUMBER: GB 9502468.3  
; FILING DATE: 09-FEB-1995  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 377 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-818-581B-4

Query Match 78.7%; Score 1523; DB 4; Length 377;  
Best Local Similarity 77.3%; Pred. No. 1.2e-158;  
Matches 283; Conservative 43; Mismatches 40; Indels 0; Gaps 0;

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Db	1	MAIPAAAFIVPISLFFMSGLVNFQAVFY	VLVLPISKDTYRRINTLVAELLWL	60
Qy	61	IDWAGVKVQIFTDHETFRMLMGKEHALV	ISNHRSDIDLVGVWSAORSGLSTLAVMK	120

Db 61 IDWAGVKVQIYTDHETFRMLGKEHALVSNHRSIDWLVGWSAQRSGCLGSLSSIAVMKK 120  
QY 121 SSKFLPVIGWSMWFSEYLFLEERSWAKDESLKSGIORLSDFPLPFWLALFVEGTRFTQAK 180  
Db 121 SSKFLPVIGWSMWFSEYLFLEERNWAKDENTLKSGLQRLNDFPKPFWLALFVEGTRFTKAK 180  
QY 181 LLAQAEYATSTGLPVPRNVLPRTKGFVSASHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240  
Db 181 LLAQAEYASAGLPVPRNVLPRTKGFVSASHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240  
QY 241 PKGQPSVVHVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDDQELQDTG 300  
Db 241 FRGKSSVVHVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDDQELQDTG 300  
QY 301 RPIKSLLVVISWACLWVAGSVKFLWSSLLSSWKGAFSAFGLAVVTALMQILIQFSQSE 360  
Db 301 RPKSLVVVSWMCLLGLGLVKFLWSSALLSSWKGMMITTFVLGIVTALMHILIRSQSE 360  
QY 361 RSNPAK 366  
Db 361 HSTPAK 366

RESULT 2  
US-08-454-267-2  
; Sequence 2, Application US/08454267  
; Patent No. 5843739  
; GENERAL INFORMATION:  
; APPLICANT: SLABAS, ANTONI R.  
; APPLICANT: BROWN, ADRIAN P.  
; TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: US  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/454,267  
; FILING DATE: 08-JUN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB93/02528  
; FILING DATE: 10-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: REED, GRANT E.  
; REGISTRATION NUMBER: P-41,264  
; REFERENCE/DOCKET NUMBER: 0623.0310000/JAG/GER  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 374 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-454-267-2

Query Match 75.0%; Score 1450.5; DB 2; Length 374;  
Best Local Similarity 70.7%; Pred. No. 1.1e-150;  
Matches 265; Conservative 51; Mismatches 58; Indels 1; Gaps 1;  
QY 1 MATAAAAVVPLGLFFASGLLVNLIQAICYVVVRPVSKSLYRRINRVVAVLLWLELVWL 60  
Db 1 MATIVVVRPVSKSLYRRINRVVAVLLWLELVWL 60

QY 61 IDWAGVKVQIYTDHETFRMLGKEHALVSNHRSIDWLVGWSAQRSGCLGSLTAVMKK 120  
Db 61 VDWAGVKVQLHADEETYSRGMKEHALIISNHRSDIDWLVGWSAQRSGCLGSLTAVMKK 120  
QY 121 SSKFLPVIGWSMWFSEYLFLEERSWAKDESLKSGIORLSDFPLPFWLALFVEGTRFTQAK 180  
Db 121 SSKFLPVIGWSMWFSEYLFLEERSWAKDESLKSGIORLSDFPLPFWLALFVEGTRFTQAK 180  
QY 181 LLAQAEYATSTGLPVPRNVLPRTKGFVSASHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240  
Db 181 LLAQAEYASAGLPVPRNVLPRTKGFVSASHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240  
QY 241 PKGQPSVVHVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDDQELQDTG 300  
Db 241 LKGQSSVVHVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDDQELQDTG 300  
QY 301 RPIKSLLVVISWACLWVAGSVKFLWSSLLSSWKGAFSAFGLAVVTALMQILIQFSQSE 360  
Db 301 RPKSLVVVSWMCLLGLGLVKFLWSSALLSSWKGMMITTFVLGIVTALMHILIRSQSE 360  
QY 361 RSNPAKIVPAKSNK 375  
Db 360 RSSSARAARNRVKE 374

RESULT 3  
US-08-454-267-6  
; Sequence 6, Application US/08454267  
; Patent No. 5843739  
; GENERAL INFORMATION:  
; APPLICANT: SLABAS, ANTONI R.  
; APPLICANT: BROWN, ADRIAN P.  
; TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: US  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/454,267  
; FILING DATE: 08-JUN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB93/02528  
; FILING DATE: 10-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: REED, GRANT E.  
; REGISTRATION NUMBER: P-41,264  
; REFERENCE/DOCKET NUMBER: 0623.0310000/JAG/GER  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 374 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-454-267-6

Query Match 75.0%; Score 1450.5; DB 2; Length 374;  
Best Local Similarity 70.7%; Pred. No. 1.1e-150;  
Matches 265; Conservative 51; Mismatches 58; Indels 1; Gaps 1;  
QY 1 MATAAAAVVPLGLFFASGLLVNLIQAICYVVVRPVSKSLYRRINRVVAVLLWLELVWL 60  
Db 1 MATIVVVRPVSKSLYRRINRVVAVLLWLELVWL 60



QY 1 MAIAAAVVPVPLGLFFASGLLVNLIQAICYVVRPVSKSLYRRINRVVAELLWLELVWL 60  
Db 1 MAIPLVVLPLGLLFLSGLIVNAIQAVLFVTIRPFKSFYRRINRFLAELLWLQLVWV 60  
QY 61 IDWAGVKVQIFTDHTETRLMGKEHALVISNHRSDIDWLGVWSAORSGLGSLTAVMKK 120  
Db 61 VDWAGVKVQLHADEETYSRSMGKEHALIISNHRSDIDWLIGWILAORSGLGSLTAVMKK 120  
QY 121 SSKFLPVIGSMWPFSEYLFELERSWAKDESTLKSGIQRSLDFFPLPFWLALFVEGTRFTQAK 180  
Db 121 SSKFLPVIGSMWPFSEYLFELERSWAKDEKTLKWGLQRLKDFPRPFWLALFVEGTRFTPAK 180  
QY 181 LLAQAEYATSTGLPVPNRNLIPTKGFVSASVSHMRSFVPAIYDVTVAIPKSSPAPTMRL 240  
Db 181 LLAQAEYASQGLPAPNRNLIPTKGFVSASVIMRDFVPAIYDVTIVPKDSPOPTMLRI 240  
QY 241 FKQPSVVHVIKRLMKELPDTDEAVAQWCRDIFVAKDALIDKHMAEGTFSQDELQDTG 300  
Db 241 LKQSSVHVHVRMKRHAMSEMPKSDSDVSKWCKDIFVAKDALIDKHMAEGTFSQDELQDTG 300  
QY 301 RPIKSLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIOFSQSE 360  
Db 300 RPVKSLVTLFWSCLLFGAIEFFKWTQLLSTWRGVAFSAFGLAVVTALMQILIOFSQAE 359  
QY 361 RSNPAKIVPAKSKNK 375  
Db 360 RSSSARAARNRVKKE 374

RESULT 4  
US-08-941-319-2  
; Sequence 2, Application US/08941319  
; Patent No. 5945323  
; GENERAL INFORMATION:  
; APPLICANT: SLABAS, ANTONI R.  
; APPLICANT: BROWN, ADRIAN P.  
; TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: US  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/941,319  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/454,267  
; FILING DATE: 08-JUN-1995  
; APPLICATION NUMBER: PCT/GB93/02528  
; FILING DATE: 10-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: REED, GRANT E.  
; REGISTRATION NUMBER: P-41,264  
; REFERENCE/DOCKET NUMBER: 0623.0310000/JAG/GER  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 374 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-941-319-2

Query Match 75.0%; Score 1450.5; DB 2; Length 374;  
Best Local Similarity 70.7%; Pred. No. 1.1e-150;  
Matches 265; Conservative 51; Mismatches 58; Indels 1; Gaps 1;  
QY 1 MAIAAAVVPVPLGLFFASGLLVNLIQAICYVVRPVSKSLYRRINRVVAELLWLELVWL 60  
Db 1 MAIPLVVLPLGLLFLSGLIVNAIQAVLFVTIRPFKSFYRRINRFLAELLWLQLVWV 60  
QY 61 IDWAGVKVQIFTDHTETRLMGKEHALVISNHRSDIDWLGVWSAORSGLGSLTAVMKK 120  
Db 61 VDWAGVKVQLHADEETYSRSMGKEHALIISNHRSDIDWLIGWILAORSGLGSLTAVMKK 120  
QY 121 SSKFLPVIGSMWPFSEYLFELERSWAKDESTLKSGIQRSLDFFPLPFWLALFVEGTRFTQAK 180  
Db 121 SSKFLPVIGSMWPFSEYLFELERSWAKDEKTLKWGLQRLKDFPRPFWLALFVEGTRFTPAK 180  
QY 181 LLAQAEYATSTGLPVPNRNLIPTKGFVSASVSHMRSFVPAIYDVTVAIPKSSPAPTMRL 240  
Db 181 LLAQAEYASQGLPAPNRNLIPTKGFVSASVIMRDFVPAIYDVTIVPKDSPOPTMLRI 240  
QY 241 FKQPSVVHVIKRLMKELPDTDEAVAQWCRDIFVAKDALIDKHMAEGTFSQDELQDTG 300  
Db 241 LKQSSVHVHVRMKRHAMSEMPKSDSDVSKWCKDIFVAKDALIDKHMAEGTFSQDELQDTG 300  
QY 301 RPIKSLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIOFSQSE 360  
Db 300 RPVKSLVTLFWSCLLFGAIEFFKWTQLLSTWRGVAFSAFGLAVVTALMQILIOFSQAE 359  
QY 361 RSNPAKIVPAKSKNK 375  
Db 360 RSSSARAARNRVKKE 374

RESULT 5  
US-08-941-319-6  
; Sequence 6, Application US/08941319  
; Patent No. 5945323  
; GENERAL INFORMATION:  
; APPLICANT: SLABAS, ANTONI R.  
; APPLICANT: BROWN, ADRIAN P.  
; TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: US  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/941,319  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/454,267  
; FILING DATE: 08-JUN-1995  
; APPLICATION NUMBER: PCT/GB93/02528  
; FILING DATE: 10-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: REED, GRANT E.  
; REGISTRATION NUMBER: P-41,264  
; REFERENCE/DOCKET NUMBER: 0623.0310000/JAG/GER  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:

LENGTH: 374 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-941-319-6

Query Match 75.0%; Score 1450.5; DB 2; Length 374;  
Best Local Similarity 70.7%; Pred. No. 1.1e-150;  
Matches 265; Conservative 51; Mismatches 58; Indels 1; Gaps 1;

QY 1 MAIAAAVVPVPLGLLFFASGLLVNLIQAICVYVVRPVSKSLYRRINRVVAELLWLVL 60  
Db 1 MAIPLVLVPLGLLFFASGLLVNLIQAICVYVVRPVSKSLYRRINRVVAELLWLVL 60  
QY 61 IDWAGVKVQIPTDHTETFLMGKEHALVISNHRSDIDWLVGVWSAQRSGCLGSLTAVMKK 120  
Db 61 VDWAGVKVQIPTDHTETFLMGKEHALVISNHRSDIDWLVGVWSAQRSGCLGSLTAVMKK 120  
QY 121 SSKFLPVIGWSMWFSEYLFLEERSWAKDESLKSGIQRSLDFPLPFWLALFVEGTRFTQAK 180  
Db 121 SSKFLPVIGWSMWFSEYLFLEERSWAKDESLKSGIQRSLDFPLPFWLALFVEGTRFTQAK 180  
QY 181 LLAQAEYATSTGLPVPNRNVLIPRTKGFVSASVSHMRSEFVPAYIDVTVAIPKSSPAPTMLRL 240  
Db 181 LLAQAEYATSTGLPVPNRNVLIPRTKGFVSASVSHMRSEFVPAYIDVTVAIPKSSPAPTMLRL 240  
QY 241 FKQPSVHVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDELODTG 300  
Db 241 LKGQSSVHVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDELODTG 300  
QY 301 RPIKSLLVVISWACLIVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE 360  
Db 301 RPKVSLVLTLFWSCLLLFGAIEFFKWTQLLSTWRGVAFSAFGLAVVTALMQILIQFSQSE 360  
QY 361 RSNPAKIVPAKSKNK 375  
Db 360 RSSSARAARNRVKKE 374

RESULT 6  
US-09-035-098-2  
Sequence 2, Application US/09035098  
Patent No. 6194640  
GENERAL INFORMATION:  
APPLICANT: SLABAS, ANTONI R.  
APPLICANT: BROWN, ADRIAN P.  
TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: US  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/035.098  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/454,267  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: REED, GRANT E.  
REGISTRATION NUMBER: P-41,264  
REFERENCE/DOCKET NUMBER: 0623.0310000/JAG/GER  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 374 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-035-098-2

Query Match 75.0%; Score 1450.5; DB 3; Length 374;  
Best Local Similarity 70.7%; Pred. No. 1.1e-150;  
Matches 265; Conservative 51; Mismatches 58; Indels 1; Gaps 1;

QY 1 MAIAAAVVPVPLGLLFFASGLLVNLIQAICVYVVRPVSKSLYRRINRVVAELLWLVL 60  
Db 1 MAIPLVLVPLGLLFFASGLLVNLIQAICVYVVRPVSKSLYRRINRVVAELLWLVL 60  
QY 61 IDWAGVKVQIPTDHTETFLMGKEHALVISNHRSDIDWLVGVWSAQRSGCLGSLTAVMKK 120  
Db 61 VDWAGVKVQIPTDHTETFLMGKEHALVISNHRSDIDWLVGVWSAQRSGCLGSLTAVMKK 120  
QY 121 SSKFLPVIGWSMWFSEYLFLEERSWAKDESLKSGIQRSLDFPLPFWLALFVEGTRFTQAK 180  
Db 121 SSKFLPVIGWSMWFSEYLFLEERSWAKDESLKSGIQRSLDFPLPFWLALFVEGTRFTQAK 180  
QY 181 LLAQAEYATSTGLPVPNRNVLIPRTKGFVSASVSHMRSEFVPAYIDVTVAIPKSSPAPTMLRL 240  
Db 181 LLAQAEYATSTGLPVPNRNVLIPRTKGFVSASVSHMRSEFVPAYIDVTVAIPKSSPAPTMLRL 240  
QY 241 FKQPSVHVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDELODTG 300  
Db 241 LKGQSSVHVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDELODTG 300  
QY 301 RPIKSLLVVISWACLIVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE 360  
Db 301 RPKVSLVLTLFWSCLLLFGAIEFFKWTQLLSTWRGVAFSAFGLAVVTALMQILIQFSQSE 360  
QY 361 RSNPAKIVPAKSKNK 375  
Db 360 RSSSARAARNRVKKE 374

RESULT 7  
US-09-035-098-6  
Sequence 6, Application US/09035098  
Patent No. 6194640  
GENERAL INFORMATION:  
APPLICANT: SLABAS, ANTONI R.  
APPLICANT: BROWN, ADRIAN P.  
TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: US  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/035.098  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/454,267  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: REED, GRANT E.  
REGISTRATION NUMBER: P-41,264

```

; REFERENCE/DOCKET NUMBER: 0623.0310000/JAG/GER
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-035-098-6

Query Match      75.0%; Score 1450.5; DB 3; Length 374;
Best Local Similarity 70.7%; Pred. No. 1.1e-150;
Matches 265; Conservative 51; Mismatches 58; Indels 1; Gaps 1;

QY 1 MAIAAAAVVPLGLLFFASGLLVNLIQAICYVVRPVSKSLYRRINRVVAELLWLELWVL 60
Db 1 MAIPLVLVPLGLLFLSGLIVNAIQAVLFTVIRPFKSFYRRINRFLAELLWLQLVWV 60
QY 61 IDWAGVKVQIFTDHTETFLMGKEHALVTSNHRSDIDWLGVWSAQSGCLGSTLAVMKK 120
Db 61 IDWAGVKVQIFTDHTETFLMGKEHALVTSNHRSDIDWLGVWSAQSGCLGSTLAVMKK 120
QY 121 SSKFLPVIWGMWFSEYLFLEERSWAKDESTLKSGIQRSLDPLPFWLALFVEGTRFTQAK 180
Db 121 SSKFLPVIWGMWFSEYLFLEERSWAKDESTLKSGIQRSLDPLPFWLALFVEGTRFTQAK 180
QY 181 LLAQAEYATSTGLPVRNVLIPTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMRL 240
Db 181 LLAQAEYATSTGLPVRNVLIPTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMRL 240
QY 241 PKQPSVVVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDOELQDTG 300
Db 241 LKGQSSVIHVTKRHSAMSEMPKSDSDVSKWCKDIFVAKDALLDKHLATGTF-DEEIRPIG 299
QY 301 RPIKSLLVVISWACLWVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMQILLIQFSQSE 360
Db 300 RPVKSLLVTLFWSCLLLFGAIEFFKWTQLLSTWRGVAFAGMALVTGVHVFIMFSQAE 359
QY 361 RSNPAKIVPAKSKNK 375
Db 360 RSSSARAARNRVKKE 374

RESULT 8
US-09-215-252-5
; Sequence 5, Application US/09215252
; Patent No. 6300487
; GENERAL INFORMATION:
; APPLICANT: LEUNG, David W.
; APPLICANT: ADOUREL, Daniel
; APPLICANT: HOLLENBACK, David
; TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE
; FILE REFERENCE: 077319/0151
; CURRENT APPLICATION NUMBER: US/09/215,252
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: US 08/618,651
; PRIOR FILING DATE: 1996-03-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Maize
US-09-215-252-5

Query Match      75.0%; Score 1450.5; DB 4; Length 374;
Best Local Similarity 70.7%; Pred. No. 1.1e-150;
Matches 265; Conservative 51; Mismatches 58; Indels 1; Gaps 1;

QY 1 MAIAAAAVVPLGLLFFASGLLVNLIQAICYVVRPVSKSLYRRINRVVAELLWLELWVL 60
Db 1 MAIPLVLVPLGLLFLSGLIVNAIQAVLFTVIRPFKSFYRRINRFLAELLWLQLVWV 60
QY 61 IDWAGVKVQIFTDHTETFLMGKEHALVTSNHRSDIDWLGVWSAQSGCLGSTLAVMKK 120
Db 61 IDWAGVKVQIFTDHTETFLMGKEHALVTSNHRSDIDWLGVWSAQSGCLGSTLAVMKK 120
QY 121 SSKFLPVIWGMWFSEYLFLEERSWAKDESTLKSGIQRSLDPLPFWLALFVEGTRFTQAK 180
Db 121 SSKFLPVIWGMWFSEYLFLEERSWAKDESTLKSGIQRSLDPLPFWLALFVEGTRFTQAK 180
QY 181 LLAQAEYATSTGLPVRNVLIPTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMRL 240
Db 181 LLAQAEYATSTGLPVRNVLIPTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMRL 240
QY 241 PKQPSVVVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDOELQDTG 300
Db 241 LKGQSSVIHVTKRHSAMSEMPKSDSDVSKWCKDIFVAKDALLDKHLATGTF-DEEIRPIG 299
QY 301 RPIKSLLVVISWACLWVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMQILLIQFSQSE 360
Db 300 RPVKSLLVTLFWSCLLLFGAIEFFKWTQLLSTWRGVAFAGMALVTGVHVFIMFSQAE 359
QY 361 RSNPAKIVPAKSKNK 375
Db 360 RSSSARAARNRVKKE 374

RESULT 9
US-09-970-989A-5
; Sequence 5, Application US/09970989A
; Patent No. 6670143
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: ADOUREL, DANIEL
; APPLICANT: HOLLENBACK, DAVID
; TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE
; FILE REFERENCE: 077319/0275
; CURRENT APPLICATION NUMBER: US/09/970,989A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/215,252
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/618,651
; PRIOR FILING DATE: 1996-03-19
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Zea mays
US-09-970-989A-5

Query Match      75.0%; Score 1450.5; DB 4; Length 374;
Best Local Similarity 70.7%; Pred. No. 1.1e-150;
Matches 265; Conservative 51; Mismatches 58; Indels 1; Gaps 1;

QY 1 MAIAAAAVVPLGLLFFASGLLVNLIQAICYVVRPVSKSLYRRINRVVAELLWLELWVL 60
Db 1 MAIPLVLVPLGLLFLSGLIVNAIQAVLFTVIRPFKSFYRRINRFLAELLWLQLVWV 60
QY 61 IDWAGVKVQIFTDHTETFLMGKEHALVTSNHRSDIDWLGVWSAQSGCLGSTLAVMKK 120
Db 61 IDWAGVKVQIFTDHTETFLMGKEHALVTSNHRSDIDWLGVWSAQSGCLGSTLAVMKK 120
QY 121 SSKFLPVIWGMWFSEYLFLEERSWAKDESTLKSGIQRSLDPLPFWLALFVEGTRFTQAK 180
Db 121 SSKFLPVIWGMWFSEYLFLEERSWAKDESTLKSGIQRSLDPLPFWLALFVEGTRFTQAK 180
QY 181 LLAQAEYATSTGLPVRNVLIPTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMRL 240
Db 181 LLAQAEYATSTGLPVRNVLIPTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMRL 240
QY 241 PKQPSVVVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDOELQDTG 300
Db 241 LKGQSSVIHVTKRHSAMSEMPKSDSDVSKWCKDIFVAKDALLDKHLATGTF-DEEIRPIG 299
QY 301 RPIKSLLVVISWACLWVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMQILLIQFSQSE 360
Db 300 RPVKSLLVTLFWSCLLLFGAIEFFKWTQLLSTWRGVAFAGMALVTGVHVFIMFSQAE 359
QY 361 RSNPAKIVPAKSKNK 375
Db 360 RSSSARAARNRVKKE 374
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Db 241 LKQSSVHVHVKRHSMPKSDDEVDVSKWCKDIFVAKDALLDKHLATGTF-DEEIRPIG 299  
QY 301 RPIKSLVVISWACLVVAGSVKFLWSSLLSSWKGVAFSAPGLAVVTALMQILIQFSQSE 360  
Db 300 RPKVSLVTLFWSCLLLFGLAIEFFKWTQLLSTWRGVAFVTAAGMALVTGVNHFVIMFSQAE 359  
QY 361 RSNPAKIVPAKSKNK 375  
Db 360 RSSSARAARNRVKKE 374

RESULT 10  
US-08-818-581B-5  
; Sequence 5, Application US/08818581B  
; Patent No. 6583340  
; GENERAL INFORMATION:  
; APPLICANT: SLABAS, Antoni Ryszard  
; APPLICANT: BROWN, Adrian Paul  
; APPLICANT: BROUGH, Clare Louise  
; APPLICANT: KROON, Johannes Theodorus Maria  
; TITLE OF INVENTION: DNA SEQUENCE ENCODING PLANT  
; TITLE OF INVENTION: 2-ACYLTRANSFERASE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: US  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/818,581B  
; FILING DATE: March 14, 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/GB96/00306  
; FILING DATE: 09-FEB-1996  
; APPLICATION NUMBER: GB 9502468.3  
; FILING DATE: 09-FEB-1995  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 375 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; ORGANISM: Zea mays  
US-08-818-581B-5

Query Match 74.5%; Score 1442.5; DB 4; Length 375;  
Best Local Similarity 70.4%; Pred. No. 8.4e-150;  
Matches 264; Conservative 51; Mismatches 59; Indels 1; Gaps 1;  
QY 1 MAIAAAVVPVPLGLFFASGLLVNLIQAICYVVRPVSKSLYRINRVVAELLWLELVWL 60  
Db 1 MAIPLVVLVPLGLLGLLVNLIQAICYVVRPVSKSLYRINRVVAELLWLELVWL 60  
QY 61 IDWAGVVKVQIFTDHETFRMLGKEHALVISNHRSDIDWLVGWVSAQSGCLGSLTAVMKK 120  
Db 61 VDWAGVVKVQLHADEETYSRSMGLHALIISNHRSDIDWLVGWVSAQSGCLGSLTAVMKK 120  
QY 121 SSKFLPVIGWSMWFSEYFLERSWAKDESTLKSGLQRLSDFPPLFWLALFVEGTRFTQAK 180  
Db 121 SSKFLPVIGWSMWFSEYFLERSWAKDEKTLKWGLQRLKDFPFWLALFVEGTRFTPAK 180  
QY 181 LLAQRYATSTGLPVRNVLIPTKGFVSVMHRSFVPAIYDVTVVAIPKSSPAPTMLRL 240  
Db 181 LLAQRYAASQGLPAPRVNLIPTKGFVSVMHRSFVPAIYDVTVVIVPKDSQPTMLRI 240

QY 241 FKQPSVHVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDOELQDTG 300  
Db 241 LKQSSVHVHVKRHSMPKSDDEVDVSKWCKDIFVAKDALLDKHLATGTF-DEEIRPIG 299  
QY 301 RPIKSLVVISWACLVVAGSVKFLWSSLLSSWKGVAFSAPGLAVVTALMQILIQFSQSE 360  
Db 300 RPKVSLVTLFWSCLLLFGLAIEFFKWTQLLSTWRGVAFVTAAGMALVTGVNHFVIMFSQAE 359  
QY 361 RSNPAKIVPAKSKNK 375  
Db 360 RSSSARAARNRVKKE 374

RESULT 11  
US-08-454-267-7  
; Sequence 7, Application US/08454267  
; Patent No. 5843739  
; GENERAL INFORMATION:  
; APPLICANT: SLABAS, ANTONI R.  
; APPLICANT: BROWN, ADRIAN P.  
; TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: US  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/454,267  
; FILING DATE: 08-JUN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB93/02528  
; FILING DATE: 10-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: REED, GRANT E.  
; REGISTRATION NUMBER: P-41,264  
; REFERENCE/DOCKET NUMBER: 0623.0310000/JAG/GER  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 295 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-454-267-7

Query Match 59.8%; Score 1156.5; DB 2; Length 295;  
Best Local Similarity 61.4%; Pred. No. 1.5e-118;  
Matches 227; Conservative 33; Mismatches 31; Indels 79; Gaps 1;  
QY 5 AAADVPLGLFFASGLLVNLIQAICYVVRPVSKSLYRINRVVAELLWLELVWLIDWW 64  
Db 4 AAADVPLGLFFASGLLVNLIQAICYVVRPVSKSLYRINRVVAELLWLELVWLIDWW 64  
QY 65 AGVKVQIFTDHETFRMLGKEHALVISNHRSDIDWLVGWVSAQSGCLGSLTAVMKKSKF 124  
Db 26 -----QSGCLGSALAVMKKSKF 44  
QY 125 LPVIGWSMWFSEYFLERSWAKDESTLKSGLQRLSDFPPLFWLALFVEGTRFTQAKLAA 184  
Db 45 LPVIGWSMWFSEYFLERSWAKDESTLKSGLQRLSDFPPLFWLALFVEGTRFTQAKLAA 104

QY 185 QEYATSTGLPVRNVLPRTKGFVS AVSHMRSFVPAIYDVTVVAIPKSSPAPTMRLRFKQ 244  
Db 105 QEYAAASSELPPVRNVLPRTKGFVS AVSNMRSFVPAIYDMTVVAIPKTSPPPTMLRLFKQ 164  
QY 245 PSVVHVHIKRLMKELPDTDEAVAQWCRDIFVAKDALLDKHAEGTFSQELQDTGRPIK 304  
Db 165 PSVVHVHIKCHSMKDLPESEDEIAQWCRDQVTKDALLDKHIAADTFAGQKEQNIGRPIK 224  
QY 305 SLLVVISWACLTVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSERSNP 364  
Db 225 SLAWLSWACLTLTGAMKFLHWSNLFSSWKGIALSALGLGIITLCMQILIRSSQSERSNP 284  
QY 365 AKIVPAKSKN 374  
Db 285 AKVAPAKPKD 294

RESULT 12  
US-08-941-319-7  
; Sequence 7, Application US/08941319  
; Patent No. 5945323  
; GENERAL INFORMATION:  
; APPLICANT: SLABAS, ANTONI R.  
; APPLICANT: BROWN, ADRIAN P.  
; TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: US  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/941,319  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/454,267  
; FILING DATE: 08-JUN-1995  
; APPLICATION NUMBER: PCT/GB93/02528  
; FILING DATE: 10-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: REED, GRANT E.  
; REGISTRATION NUMBER: P-41,264  
; REFERENCE/DOCKET NUMBER: 0623.0310000/JAG/GER  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 295 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-941-319-7

Query Match 59.8%; Score 1156.5; DB 2; Length 295;  
Best Local Similarity 61.4%; Pred. No. 1.5e-118;  
Matches 227; Conservative 33; Mismatches 31; Indels 79; Gaps 1;  
QY 5 AAADVVPGLGLFFASGLLVNLITQAICYVVVRPVSKSLYRRINRVVAELLWLELVWLDWW 64  
Db 4 AAADVVPGLGLFFISGLVNVLL-----  
QY 65 AGVKVQIFTDHTFRLMGKEHALVISNHRSDIDLWVGWVSAQRSGCLGSTLAWMKSSKF 124  
Db 26 -----QRSGCLGSALAVMKSSKF 44

QY 125 LPVIGWSMWFSEYLFELRSWAKDESTLKSGIQRSLDFPLPFWLALFVEGTRETQAKLLAA 184  
Db 45 LPVIGWSMWFSEYLFELERNWAKDESTLKSGIQRSLNDFPRPFWLALFVEGTRETQAKLLAA 104  
QY 185 QEYATSTGLPVRNVLPRTKGFVS AVSHMRSFVPAIYDVTVVAIPKSSPAPTMRLRFKQ 244  
Db 105 QEYAAASSELPPVRNVLPRTKGFVS AVSNMRSFVPAIYDMTVVAIPKTSPPPTMLRLFKQ 164  
QY 245 PSVVHVHIKRLMKELPDTDEAVAQWCRDIFVAKDALLDKHAEGTFSQELQDTGRPIK 304  
Db 165 PSVVHVHIKCHSMKDLPESEDEIAQWCRDQVTKDALLDKHIAADTFAGQKEQNIGRPIK 224  
QY 305 SLLVVISWACLTVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSERSNP 364  
Db 225 SLAWLSWACLTLTGAMKFLHWSNLFSSWKGIALSALGLGIITLCMQILIRSSQSERSNP 284  
QY 365 AKIVPAKSKN 374  
Db 285 AKVAPAKPKD 294

RESULT 13  
US-09-035-098-7  
; Sequence 7, Application US/09035098  
; Patent No. 6194640  
; GENERAL INFORMATION:  
; APPLICANT: SLABAS, ANTONI R.  
; APPLICANT: BROWN, ADRIAN P.  
; TITLE OF INVENTION: DNA ENCODING 2-ACYLTRANSFERASES  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: US  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/035,098  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/454,267  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: REED, GRANT E.  
; REGISTRATION NUMBER: P-41,264  
; REFERENCE/DOCKET NUMBER: 0623.0310000/JAG/GER  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 295 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-035-098-7

Query Match 59.8%; Score 1156.5; DB 3; Length 295;  
Best Local Similarity 61.4%; Pred. No. 1.5e-118;  
Matches 227; Conservative 33; Mismatches 31; Indels 79; Gaps 1;  
QY 5 AAADVVPGLGLFFASGLLVNLITQAICYVVVRPVSKSLYRRINRVVAELLWLELVWLDWW 64  
Db 4 AAADVVPGLGLFFISGLVNVLL-----  
25

QY 65 AGVKVQIFTDHETFRMLMGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSLTAVMKKSKF 124  
Db 26 -----Q-RSGCLGSALAVMKKSKF 44  
QY 125 LPVIGWSMWFSEYLFLEERSWAKDESTLKSIGIQRSLDPFLPFWLALFVEGTRFTQAKLLAA 184  
Db 45 LPVIGWSMWFSEYLFLEERNWAKDESTLKSIGIQRSLDPFLPFWLALFVEGTRFTQAKLLAA 104  
QY 185 QEYATSTGLPVRNVLIPRTKGFVSASVSHMRSFVPAIYDVTVAIPKSSPAPTMLRPFKGQ 244  
Db 105 QEYAAASSELPPVRNVLIPRTKGFVSASVSHMRSFVPAIYDVTVAIPKSSPAPTMLRPFKGQ 164  
QY 245 PSVVHVHIKRLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTSDQELQDTGRPIK 304  
Db 165 PSVVHVHIKCHSMKOLPESEDEIAQWCRDQFVTKDALLDKHIAADTFAGQKEQNIQGRPIK 224  
QY 305 SLLVVISWACLAVVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMQLIILQFSQSERSNP 364  
Db 225 SLAVVLSWACLLTLGAMKFLHWSNLFSSWKGIALSALGLGIITLCMQILIRSSQSERSSTP 284  
QY 365 AKIVPAKSKN 374  
Db 285 AKVAPAKPKD 294

RESULT 14

US-08-818-581B-6  
; Sequence 6, Application US/08818581B  
; Patent No. 6583340  
; GENERAL INFORMATION:  
; APPLICANT: SLABAS, Antoni Ryszard  
; APPLICANT: BROWN, Adrian Paul  
; APPLICANT: BROUGH, Clare Louise  
; APPLICANT: KROON, Johannes Theodorus Maria  
; TITLE OF INVENTION: DNA SEQUENCE ENCODING PLANT  
; TITLE OF INVENTION: 2-ACYLTRANSFERASE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: US  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/818,581B  
; FILING DATE: March 14, 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/GB96/00306  
; FILING DATE: 09-FEB-1996  
; APPLICATION NUMBER: GB 9502468.3  
; FILING DATE: 09-FEB-1995  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 311 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; ORGANISM: Brassica napus  
; US-08-818-581B-6  
Query Match 59.8%; Score 1156.5; DB 4; Length 311;  
Best Local Similarity 61.4%; Pred. No. 1.7e-118;  
Matches 227; Conservative 33; Mismatches 31; Indels 79; Gaps 1;

Db 4 AAIVVPLGILFFISGLVNNL----- 25  
QY 65 AGVKVQIFTDHETFRMLMGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSLTAVMKKSKF 124  
Db 26 -----Q-RSGCLGSALAVMKKSKF 44  
QY 125 LPVIGWSMWFSEYLFLEERSWAKDESTLKSIGIQRSLDPFLPFWLALFVEGTRFTQAKLLAA 184  
Db 45 LPVIGWSMWFSEYLFLEERNWAKDESTLKSIGIQRSLDPFLPFWLALFVEGTRFTQAKLLAA 104  
QY 185 QEYATSTGLPVRNVLIPRTKGFVSASVSHMRSFVPAIYDVTVAIPKSSPAPTMLRPFKGQ 244  
Db 105 QEYAAASSELPPVRNVLIPRTKGFVSASVSHMRSFVPAIYDVTVAIPKSSPAPTMLRPFKGQ 164  
QY 245 PSVVHVHIKRLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTSDQELQDTGRPIK 304  
Db 165 PSVVHVHIKCHSMKOLPESEDEIAQWCRDQFVTKDALLDKHIAADTFAGQKEQNIQGRPIK 224  
QY 305 SLLVVISWACLAVVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMQLIILQFSQSERSNP 364  
Db 225 SLAVVLSWACLLTLGAMKFLHWSNLFSSWKGIALSALGLGIITLCMQILIRSSQSERSSTP 284  
QY 365 AKIVPAKSKN 374  
Db 285 AKVAPAKPKD 294

RESULT 15

US-09-215-252-13  
; Sequence 13, Application US/09215252  
; Patent No. 6300487  
; GENERAL INFORMATION:  
; APPLICANT: LEUNG, David W.  
; APPLICANT: ADOUREL, Daniel  
; APPLICANT: HOLLENBACK, David  
; TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE  
; FILE REFERENCE: 077319/0151  
; CURRENT APPLICATION NUMBER: US/09/215,252  
; CURRENT FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: US 08/618,651  
; PRIOR FILING DATE: 1996-03-19  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 376  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-215-252-13  
Query Match 32.5%; Score 628; DB 4; Length 376;  
Best Local Similarity 37.6%; Pred. No. 2.7e-60;  
Matches 127; Conservative 75; Mismatches 124; Indels 12; Gaps 4;  
QY 12 LGLLFFASGLLVNLIQAICYVVRVPSKSLYRRINRVVAELLWLELVLDWAGVKVQI 71  
Db 17 VGFVVFVSGLVINFVQ-LCTLALVPVSKQLYRRNCLRLAYSLWSQLVLMLEWWSCTECTL 75  
QY 72 FTDHETFRMLMGKEHALVISNHRSDIDWLVGWVSAQRSGCLGSLTAVMKKSKFLPVIGWS 131  
Db 76 FTDQATVERFEGKEHAIVILNHNFEIDFLCGWTMCERFGLGSSKVLAKKELLYVPLIGWT 135  
QY 132 MWFSEYLFLEERSWAKDESTLKSIGIQRSLDPFLPFWLALFVEGTRFTQAKLLAAQYATST 191  
Db 136 WYFLEIVFCKRKEEDRTVVEGLRLSDYPEYMWFLYCEGTRFTETKRVSMVEAAK 195  
QY 192 GLPVRNVLIPRTKGFVSASVSHMRSFVPAIYDVTVAIPKSSPAPTMLRPFKGQSVVHVH 251  
Db 196 GLPVLKYHLLPRTKGTAVKCLRGTVAAVYDVTNLF-RGNKNPSSLGILYKGYEADM 254  
QY 252 IKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTSDQELQDTGRPIKSLLVVIS 311  
Db 255 VRRFPLEIDPEKEAAQWLHKLQYQKDALQEIYVQKGMFPGEQCFKPARRP-WTLNLF 313



Qy 312 WACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTAL 349  
Db 314 WATILL-----SPLFSFVLGVFASGSPLLILITFL 342

Search completed: July 7, 2004, 13:42:25  
Job time : 24 secs



OM protein - protein search, using sw model

Run on: July 7, 2004, 13:33:02 / Search time 59 Seconds  
(without alignments)  
1805.431 Million cell updates/sec

Title: US-09-914-098-56  
Perfect score: 1935  
Sequence: 1 MAIAAAAVVPLGLFFASG.....QSERSNPAKIVPAKSKNKG 377

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

1:	geneseqp1980s.*
2:	geneseqp1990s.*
3:	geneseqp2000s.*
4:	geneseqp2001s.*
5:	geneseqp2002s.*
6:	geneseqp2003as.*
7:	geneseqp2003bs.*
8:	geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		DB ID	Description
		Match	Length		
1	1935	100.0	377	3	AAB08478 Nucleotid
2	1609.5	83.2	387	3	AAY99482 Jojoba ac
3	1570	81.1	389	3	AAY99473 Arabidops
4	1570	81.1	389	3	AAG51310 Arabidops
5	1564	80.8	389	3	AAG13219 Arabidops
6	1504	77.7	377	2	AAR99249 Limnanthe
7	1453.5	75.1	360	3	AAG51330 Arabidops
8	1453.5	75.1	374	2	AAR59712 Maize 2-a
9	1450.5	75.0	374	4	AAU00667 Maize lys
10	1450.5	75.0	374	5	AAE15288 Maize LPA
11	1431.5	74.0	374	3	AAB08477 Amino aci
12	1414.5	73.1	374	3	AAB08479 Amino aci
13	1277	66.0	376	3	AAG31593 Arabidops
14	1246	64.4	310	3	AAG51311 Arabidops
15	1240	64.1	310	3	AAG13220 Arabidops
16	1155.5	59.7	294	3	AAG33441 Zea mays
17	1147.5	59.3	295	2	AAR59713 Rapeseed
18	1129.5	58.4	281	3	AAG51331 Arabidops
19	1068	55.2	273	3	AAG51312 Arabidops
20	1062	54.9	273	3	AAG13221 Arabidops
21	967.5	50.0	257	3	AAG33442 Zea mays
22	958.5	49.5	240	4	AAB75581 Gene 29 h
23	951.5	49.2	244	3	AAG51332 Arabidops
24	893.5	46.2	243	3	AAG33443 Zea mays
25	889	45.9	273	3	AAG31584 Arabidops

26	836	43.2	259	3	AAG31585 Arabidops
27	628	32.5	353	4	AAM39793 Human pol
28	628	32.5	368	3	AAY99422 Human PRO
29	628	32.5	368	4	AAB66171 Protein o
30	628	32.5	368	4	AAY99422 Human PRO
31	628	32.5	368	6	ABU58568 Human PRO
32	628	32.5	368	6	ABU88116 Novel hum
33	628	32.5	368	6	ABU84431 Human sec
34	628	32.5	368	6	ABR66305 Human sec
35	628	32.5	368	6	ABR65695 Human sec
36	628	32.5	368	6	ABU99635 Human sec
37	628	32.5	368	6	ABU82874 Human PRO
38	628	32.5	368	6	ABU89995 Novel hum
39	628	32.5	368	6	ABR68244 Human sec
40	628	32.5	368	6	ABU96297 Novel hum
41	628	32.5	368	6	ABU92728 Human sec
42	628	32.5	368	6	ABO08805 Human sec
43	628	32.5	368	6	ABO02857 Human sec
44	628	32.5	368	6	ABR75011 Human sec
45	628	32.5	368	6	ABR94773 Human sec

ALIGNMENTS

RESULT 1  
AAB08478  
ID AAB08478 standard; protein; 377 AA.

XX AAB08478;

XX 20-DEC-2000 (first entry)

XX Nucleotide sequence of a lysophosphatidic acid acetyltransferase.

XX Lysophosphatidic acid acetyltransferase; LPAAT; transgenic plant;  
XX triacylglycerol; oil content.

XX Glycine max.

XX WO200049156-A2.

XX 24-AUG-2000.

XX 22-FEB-2000; 2000WO-US004526.

XX 22-FEB-1999; 99US-0121119P.

XX (DUPO ) DU PONT DE NEMOURS & CO E I.

XX Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ, Ripp KG;

XX WPI; 2000-558300/51.

XX N-PSDB; AAA64200.

XX New nucleic acid fragment encoding a lysophosphatidic acid  
XX acetyltransferase (LPAAT) isozyme, useful for creating transgenic plants  
XX which encode LPAAT at higher or lower levels than normal.

XX Claim 31; Page 99-100; 102pp; English.

XX The present sequence represents a lysophosphatidic acid acetyltransferase  
XX (LPAAT) isoenzyme. The nucleic acid may be used to create transgenic  
XX plants which encode LPAAT at higher or lower levels than normal or in  
XX cell types or developmental stages in which they are not normally found.  
XX This would have the effect of altering the level of specific  
XX triacylglycerols in those cells, for e.g. overexpression of an LPAAT  
XX similar to the maize LPAAT will result in higher oil content in the seed,  
XX stem and leaf. LPAAT chimeric genes may be used for co-suppression of  
XX genes encoding LPAAT. The polynucleotides may also be used as probes for  
XX genetically and physically mapping the genes that are a part of, and as  
XX markers for traits linked to those genes

SQ Sequence 377 AA;  
Query Match 100.0%; Score 1935; DB 3; Length 377;  
Best Local Similarity 100.0%; Pred. No. 4e-194;  
Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAIAAAVVVPLGLFFASGLLVNLIQAICVYVVRPVSKSLYRRINRVVAELLWLELWL 60  
DB 1 MAIAAAVVVPLGLFFASGLLVNLIQAICVYVVRPVSKSLYRRINRVVAELLWLELWL 60  
QY 61 IDWAGVKVQIFTDHETFRMLGKEHALVISNHRSDIDLVGWVSAQSGCLGSTLAVMKK 120  
DB 61 IDWAGVKVQIFTDHETFRMLGKEHALVISNHRSDIDLVGWVSAQSGCLGSTLAVMKK 120  
QY 121 SSKFLPVIWGMWVFSEYLFLEERSWAKDESTLKSGIQRSLDFPLPFWLALFVEGTRFTQAK 180  
DB 121 SSKFLPVIWGMWVFSEYLFLEERSWAKDESTLKSGIQRSLDFPLPFWLALFVEGTRFTQAK 180  
QY 181 LLAQAEYATSTGLPVRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240  
DB 181 LLAQAEYATSTGLPVRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240  
QY 241 FKGPSTVHVHIKRLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQELQDTG 300  
DB 241 FKGPSTVHVHIKRLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQELQDTG 300  
QY 301 RPIKSLLVVISWACLWVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE 360  
DB 301 RPIKSLLVVISWACLWVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE 360  
QY 361 RSNPAKIVPAKSKNKS 377  
DB 361 RSNPAKIVPAKSKNKS 377

RESULT 2  
AA99482  
ID AA99482 standard; protein; 387 AA.  
AC AA99482;  
XX 15-AUG-2000 (first entry)  
DT Jojoba acyltransferase LPAAT, SEQ ID NO:162.  
DE Lysophosphatidic acid acyltransferase; LPAAT; jojoba; lipid synthesis;  
KW recombinant expression; membrane fluidity; cold resistance;  
KW transgenic plant.  
XX Simmondsia chinensis.  
OS

Key Location/Qualifiers  
FT Misc-difference 40 /note= "Encoded by NNTACA"  
XX  
PN WO200018889-A2.  
XX  
PD 06-APR-2000.  
XX  
PF 24-SEP-1999; 99WO-US022231.  
XX  
PR 25-SEP-1998; 98US-0101939P.  
XX  
PA (CALJ ) CALGENE LLC.  
XX  
PI Lassner MW, Emig RA, Ruezinsky DM, Van Eenennaam A;  
XX WPI; 2000-303447/26.  
DR N-PSDB; AAA37472.  
XX  
PT Novel acyltransferase related proteins useful for altering membrane  
XX fluidity in plant cells e.g. to induce chill tolerance.

PS Example 5; Page 98-99; 126pp; English.  
XX The invention relates to nucleic acids encoding novel plant  
CC acyltransferase-like proteins (AAA37343-A37445) which comprise one of 8  
CC conserved acyltransferase motifs (AA99474-Y99481). Acyltransferases  
CC catalyze the transfer of acyl groups from a donor to a variety of  
CC substrates such as glycerides, sterols, stanols and phosphatides. Such  
CC enzymes play a key role in lipid synthesis, and thereby affect the  
CC characteristics of the plant. For example, cold-hardened plants have  
CC different lipid concentrations in the cell membrane compared to non-  
CC hardened plants, which makes the membrane more fluid and the plant more  
CC tolerant of low temperatures. The nucleic acid sequences of the invention  
CC can be used as probes or for expressing acyltransferase-like proteins in  
CC host cells e.g., for recombinant protein production. They may be  
CC expressed in plant cells to alter the lipid composition of the plant  
CC e.g., for the production of chill-resistant plants, or for altering the  
CC composition of plant oils. The present sequence represents jojoba  
CC lysophosphatidic acid acyltransferase (LPAAT)

XX Sequence 387 AA;  
SQ  
Query Match 83.2%; Score 1609.5; DB 3; Length 387;  
Best Local Similarity 81.3%; Pred. No. 6.5e-160;  
Matches 304; Conservative 29; Mismatches 40; Indels 1; Gaps 1;  
QY 1 MAIAAAVVVPLGLFFASGLLVNLIQAICVYVVRPVSKSLYRRINRVVAELLWLELWL 60  
DB 1 MGIPAAAVIVPLGLFFSGLFINFICAICFVLVRPLSKT-YRRINRVVLELLWLELWL 59  
QY 61 IDWAGVKVQIFTDHETFRMLGKEHALVISNHRSDIDLVGWVSAQSGCLGSTLAVMKK 120  
DB 60 VDWWASVKIKLFTDPTFRMLGKEHALVISNHRSDIDLVGWVLAQSGCLGSTLAVMKK 119  
QY 121 SSKFLPVIWGMWVFSEYLFLEERSWAKDESTLKSGIQRSLDFPLPFWLALFVEGTRFTQAK 180  
DB 120 SSKFLPVIWGMWVFSEYLFLEERSWAKDESTLKSGIQRSLDFPLPFWLALFVEGTRFTQAK 179  
QY 181 LLAQAEYATSTGLPVRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240  
DB 180 LLAQAEYATSMGLPVRNVLIPRTKGFVSAVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL 239  
QY 241 FKGPSTVHVHIKRLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQELQDTG 300  
DB 240 FKGPSTVHVHIKRRSMKDLPEAADDVAQWCRDITFVAKDALLDKHNVDDTFGDEYLQDTG 299  
QY 301 RPIKSLLVVISWACLWVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE 360  
DB 300 RPLKSLFVAVSWALILGLKFLRWSSLLSSWKGVAFSAACLVVVTILMQILIQFSQSE 359  
QY 361 RSNPAKIVPAKSKN 374  
DB 360 RSTPAKVAPGPKPN 373

RESULT 3  
AA99473  
ID AA99473 standard; protein; 389 AA.  
XX  
AC AA99473;  
XX  
DT 15-AUG-2000 (first entry)  
XX  
DE Arabidopsis thaliana acyltransferase ATLPAAT1.  
XX  
KW Lysophosphatidic acid acyltransferase; ATLPAAT1; lipid synthesis;  
KW recombinant expression; membrane fluidity; cold resistance;  
XX transgenic plant.  
OS Arabidopsis thaliana.  
XX  
PN WO200018889-A2.  
XX

XX	AAG51310;	
XX	AC	
XX	DT	18-OCT-2000 (first entry)
XX	DE	Arabidopsis thaliana protein fragment SEQ ID NO: 65110.
XX	KW	Protein identification; signal transduction pathway; metabolic pathway;
XX	KW	hybridisation assay; genetic mapping; gene expression control; promoter;
XX	KW	termination sequence.
XX	OS	Arabidopsis thaliana.
XX	PN	EP1033405-A2.
XX	PD	06-SEP-2000.
XX	PF	25-FEB-2000; 2000EP-00301439.
XX	PR	25-FEB-1999; 99US-0121825P.
PR	PR	05-MAR-1999; 99US-0123180P.
PR	PR	09-MAR-1999; 99US-0123548P.
PR	PR	23-MAR-1999; 99US-0125788P.
PR	PR	25-MAR-1999; 99US-0126264P.
PR	PR	29-MAR-1999; 99US-0126785P.
PR	PR	01-APR-1999; 99US-0127462P.
PR	PR	06-APR-1999; 99US-0128234P.
PR	PR	08-APR-1999; 99US-0128714P.
PR	PR	16-APR-1999; 99US-0129845P.
PR	PR	19-APR-1999; 99US-0130077P.
PR	PR	21-APR-1999; 99US-0130449P.
PR	PR	23-APR-1999; 99US-0130510P.
PR	PR	23-APR-1999; 99US-0130891P.
PR	PR	28-APR-1999; 99US-0131449P.
PR	PR	30-APR-1999; 99US-0132048P.
PR	PR	30-APR-1999; 99US-0132407P.
PR	PR	04-MAY-1999; 99US-0132484P.
PR	PR	05-MAY-1999; 99US-0132485P.
PR	PR	06-MAY-1999; 99US-0132486P.
PR	PR	06-MAY-1999; 99US-0132487P.
PR	PR	07-MAY-1999; 99US-0132863P.
PR	PR	11-MAY-1999; 99US-0134256P.
PR	PR	14-MAY-1999; 99US-0134218P.
PR	PR	14-MAY-1999; 99US-0134219P.
PR	PR	14-MAY-1999; 99US-0134221P.
PR	PR	14-MAY-1999; 99US-0134370P.
PR	PR	18-MAY-1999; 99US-0134768P.
PR	PR	19-MAY-1999; 99US-0134941P.
PR	PR	20-MAY-1999; 99US-0135124P.
PR	PR	21-MAY-1999; 99US-0135353P.
PR	PR	24-MAY-1999; 99US-0135629P.
PR	PR	25-MAY-1999; 99US-0136021P.
PR	PR	27-MAY-1999; 99US-0136392P.
PR	PR	28-MAY-1999; 99US-0136782P.
PR	PR	01-JUN-1999; 99US-0137222P.
PR	PR	03-JUN-1999; 99US-0137528P.
PR	PR	04-JUN-1999; 99US-0137502P.
PR	PR	07-JUN-1999; 99US-0137724P.
PR	PR	08-JUN-1999; 99US-0138094P.
PR	PR	10-JUN-1999; 99US-0138540P.
PR	PR	10-JUN-1999; 99US-0138847P.
PR	PR	14-JUN-1999; 99US-0139119P.
PR	PR	16-JUN-1999; 99US-0139452P.
PR	PR	16-JUN-1999; 99US-0139455P.
PR	PR	16-JUN-1999; 99US-0139453P.
PR	PR	17-JUN-1999; 99US-0139454P.
PR	PR	18-JUN-1999; 99US-0139456P.
PR	PR	18-JUN-1999; 99US-0139457P.
PR	PR	18-JUN-1999; 99US-0139458P.
PR	PR	18-JUN-1999; 99US-0139459P.
PR	PR	18-JUN-1999; 99US-0139460P.
PR	PR	18-JUN-1999; 99US-0139461P.

PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
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PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.

PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
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PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 14-OCT-1999; 99US-0159329P.  
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PR 14-OCT-1999; 99US-0159637P.  
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PR 21-OCT-1999; 99US-0160741P.  
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PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 81.1%; Score 1570; DB 3; Length 389;  
Best Local Similarity 77.2%; Pred. No. 9.2e-156;  
Matches 287; Conservative 43; Mismatches 42; Indels 0; Gaps 0;

QY 3 IAAA... 62  
Db 2 VIAA... 61  
QY 63 WAGV... 122  
Db 62 WAGV... 121  
QY 123 KFLP... 182  
Db 122 KFLP... 181  
QY 183 AAQE... 242



```
QY      243  GQPSVVHVIKRLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDELODTGRP 302
Db      242  GQPSVVHVIKCHSMKDLPESSDDAIAQWCRDQFVAKDALLDKHIAADTFPGQEQEIGNGRP 301
QY      303  IKSLLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTTALMOILIQFSQSERS 362
Db      302  IKSLAVLVSWACVLTGLGAIKFLHWAQLFSSWKGITITISALGLGIITILCMQILIRSSQSERS 361
QY      363  NPAKIVPAKSN 374
Db      362  TPAKVVPKPKD 373

RESULT 5
AAG13219
ID  AAG13219 standard; protein; 389 AA.
XX
AC  AAG13219;
XX
DT  17-OCT-2000 (first entry)
XX
DE  Arabidopsis thaliana protein fragment SEQ ID NO: 12633.
KW  protein identification; signal transduction pathway; metabolic pathway;
KW  hybridisation assay; genetic mapping; gene expression control; promoter;
KW  termination sequence.
OS  Arabidopsis thaliana.
XX
PN  EP1033405-A2.
PD
XX  06-SEP-2000.
PF
XX  25-FEB-2000; 2000EP-00301439.
XX
PR  25-FEB-1999; 99US-0121825P.
PR  05-MAR-1999; 99US-0123180P.
PR  09-MAR-1999; 99US-0123548P.
PR  23-MAR-1999; 99US-0125788P.
PR  25-MAR-1999; 99US-0126264P.
PR  29-MAR-1999; 99US-0126785P.
PR  01-APR-1999; 99US-0127462P.
PR  06-APR-1999; 99US-0128234P.
PR  08-APR-1999; 99US-0128714P.
PR  16-APR-1999; 99US-0129845P.
PR  19-APR-1999; 99US-0130077P.
PR  21-APR-1999; 99US-0130449P.
PR  23-APR-1999; 99US-0130510P.
PR  23-APR-1999; 99US-0130891P.
PR  28-APR-1999; 99US-0131449P.
PR  30-APR-1999; 99US-0132048P.
PR  30-APR-1999; 99US-0132407P.
PR  04-MAY-1999; 99US-0132484P.
PR  05-MAY-1999; 99US-0132485P.
PR  06-MAY-1999; 99US-0132486P.
PR  07-MAY-1999; 99US-0132863P.
PR  11-MAY-1999; 99US-0134256P.
PR  14-MAY-1999; 99US-0134218P.
PR  14-MAY-1999; 99US-0134219P.
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PR  14-MAY-1999; 99US-0134370P.
PR  18-MAY-1999; 99US-0134768P.
PR  19-MAY-1999; 99US-0134941P.
PR  20-MAY-1999; 99US-0135124P.
PR  21-MAY-1999; 99US-0135353P.
PR  24-MAY-1999; 99US-0135629P.
PR  25-MAY-1999; 99US-0136021P.
PR  27-MAY-1999; 99US-0136392P.
PR  28-MAY-1999; 99US-0136782P.
PR  01-JUN-1999; 99US-0137222P.
PR  03-JUN-1999; 99US-0137528P.
PR  04-JUN-1999; 99US-0137502P.
PR  07-JUN-1999; 99US-0137724P.
PR  08-JUN-1999; 99US-0138094P.
PR  10-JUN-1999; 99US-0138540P.
PR  10-JUN-1999; 99US-0138847P.
PR  14-JUN-1999; 99US-0139119P.
PR  16-JUN-1999; 99US-0139452P.
PR  17-JUN-1999; 99US-0139492P.
PR  18-JUN-1999; 99US-0139454P.
PR  18-JUN-1999; 99US-0139455P.
PR  18-JUN-1999; 99US-0139456P.
PR  18-JUN-1999; 99US-0139457P.
PR  18-JUN-1999; 99US-0139458P.
PR  18-JUN-1999; 99US-0139459P.
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PR  18-JUN-1999; 99US-0139461P.
PR  18-JUN-1999; 99US-0139462P.
PR  18-JUN-1999; 99US-0139463P.
PR  18-JUN-1999; 99US-0139750P.
PR  18-JUN-1999; 99US-0139763P.
PR  21-JUN-1999; 99US-0139817P.
PR  22-JUN-1999; 99US-0139899P.
PR  23-JUN-1999; 99US-0140353P.
PR  23-JUN-1999; 99US-0140354P.
PR  24-JUN-1999; 99US-0140695P.
PR  28-JUN-1999; 99US-0140823P.
PR  29-JUN-1999; 99US-0140991P.
PR  30-JUN-1999; 99US-0141287P.
PR  01-JUL-1999; 99US-0141842P.
PR  01-JUL-1999; 99US-0142154P.
PR  02-JUL-1999; 99US-0142055P.
PR  06-JUL-1999; 99US-0142390P.
PR  08-JUL-1999; 99US-0142803P.
PR  09-JUL-1999; 99US-0142920P.
PR  12-JUL-1999; 99US-0142977P.
PR  13-JUL-1999; 99US-0143542P.
PR  14-JUL-1999; 99US-0143624P.
PR  15-JUL-1999; 99US-0144005P.
PR  16-JUL-1999; 99US-0144085P.
PR  16-JUL-1999; 99US-0144086P.
PR  19-JUL-1999; 99US-0144325P.
PR  19-JUL-1999; 99US-0144331P.
PR  19-JUL-1999; 99US-0144332P.
PR  19-JUL-1999; 99US-0144333P.
PR  19-JUL-1999; 99US-0144334P.
PR  19-JUL-1999; 99US-0144335P.
PR  20-JUL-1999; 99US-0144352P.
PR  20-JUL-1999; 99US-0144632P.
PR  20-JUL-1999; 99US-0144884P.
PR  21-JUL-1999; 99US-0144814P.
PR  21-JUL-1999; 99US-0145086P.
PR  21-JUL-1999; 99US-0145088P.
PR  22-JUL-1999; 99US-0145085P.
PR  22-JUL-1999; 99US-0145087P.
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PR  22-JUL-1999; 99US-0145192P.
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PR  23-JUL-1999; 99US-0145218P.
PR  23-JUL-1999; 99US-0145224P.
PR  26-JUL-1999; 99US-0145276P.
PR  27-JUL-1999; 99US-0145913P.
PR  27-JUL-1999; 99US-0145918P.
PR  27-JUL-1999; 99US-0145919P.
PR  28-JUL-1999; 99US-0145951P.
PR  02-AUG-1999; 99US-0146386P.
PR  02-AUG-1999; 99US-0146388P.
PR  02-AUG-1999; 99US-0146389P.
PR  03-AUG-1999; 99US-0147038P.
PR  04-AUG-1999; 99US-0147204P.
PR  04-AUG-1999; 99US-0147302P.
PR  05-AUG-1999; 99US-0147192P.
PR  05-AUG-1999; 99US-0147260P.
```



PT improved oil prodn.  
XX Example 2; Fig 1; 54pp; English.  
PS  
XX  
CC The amino acid sequence (AAR99249) was deduced of Limnanthes clone 1  
CC (AAT35205), a cDNA clone obtd. by heterologous screening of a Limnanthes  
CC douglasii seed cDNA library using a 600 bp NcoI/PstI fragment of a rape 2  
CC -acyltransferase (2AT) clone corresponding to the N-terminus of the rape  
CC protein. Another isolated clone (AAT35204) codes for Limnanthes 2AT  
CC (AAR99248), which can be used to increase the erucic acid content of  
CC transgenic plants  
XX  
SQ Sequence 377 AA;  
  
Query Match 77.7%; Score 1504; DB 2; Length 377;  
Best Local Similarity 76.2%; Pred. No. 7.5e-149;  
Matches 279; Conservative 45; Mismatches 42; Indels 0; Gaps 0;  
  
Qy 1 MAIAAAVVVPLGLLFFASGLLVNLIQAICYVVVRPVYKSLYRRINRVVAELLWLELVL 60  
Db 1 MAIPAAAFIVPISLLFFNSGLVNFVFIQAVFYVLRPISKDTYRRINTLVAEELLWLELWV 60  
  
Qy 61 IDWAGVKVQIETDHEFRLMGKEHALVISNHRSDIDWLVGWSAQBSGCLGSTLAVMKK 120  
Db 61 IDWAGVKVQLYTDTESFELMRKEHALICNHRSDIDWLVGWLQRCGCLSSSIAMVKK 120  
  
Qy 121 SSKFLPVIGWSMWFSEYLFELERSWAKDESTLKSIGIQLSDDEPLPFMLALFVEGTRFTQAK 180  
Db 121 SSKFLPVIGWSMWFSEYLFELKRNWAKDENTLKSGLQRLNDFPKPFMLALFVEGTRFTKAK 180  
  
Qy 181 LLAAQEQYATSTGLPVPRNVLIPTKGFVSASVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240  
Db 181 LLAAQEQYAAAGLPVPRNVLIPTKGFVSASVSNMRSFVPAIYDLTVAIPKTEQPTMLRL 240  
  
Qy 241 FKQPSVVHVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDOELQDTG 300  
Db 241 FRGKSSVVHVHVKRHLMKDPKPTDDGVAQWCKDQFISKDALLDKHVAEDTFSGLEVDIG 300  
  
Qy 301 RPIKSLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQSE 360  
Db 301 RPMKSLVVVSWMCLLCLGLVKFLQWSALLSSWKGMITTFVLGIVTALMHMLIRSSQSE 360  
  
Qy 361 RSNPAK 366  
Db 361 HSTPAK 366  
  
RESULT 7  
AAG51330  
ID AAG51330 standard; protein; 360 AA.  
XX  
XX AAG51330;  
AC  
DT 18-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65137.  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-00301439.  
XX  
PR 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
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PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
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PR 07-MAY-1999; 99US-0132863P.  
PR 11-MAY-1999; 99US-0134256P.  
PR 14-MAY-1999; 99US-0134218P.  
PR 14-MAY-1999; 99US-0134219P.  
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PR 24-MAY-1999; 99US-0135629P.  
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PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
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PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.



DE		Maize 2-acyltransferase.
XX		
KW		2-Acyltransferase; lipid; oilseed; Escherichia coli; transgenic plant;
KW		crop improvement.
XX		
OS		Zea mays.
XX		
XX		WO9413814-A1.
PD		23-JUN-1994.
XX		
PX		10-DEC-1993; 93WO-GB002528.
XX		
PX		10-DEC-1992; 92GB-00025845.
XX		(NICK-) NICKERSON BIOCHEM LTD.
PA		
XX		Slabas AR, Brown AP;
PI		
XX		WPI; 1994-217888/26.
DR		N-PSDB; AAQ68267.
DR		
XX		
PT		DNA encoding a plant 2-acryl-transferase - used to produce plants with
PT		increased or decreased lipid levels and with a tailored lipid compsn.
XX		
PX		Disclosure; Fig 1; 45pp; English.
PS		
CC		Complementation studies using a maize cDNA library transferred into E.
CC		coli JC201 allowed the isolation of a plasmid encoding a 2-
CC		acyltransferase enzyme from maize. DNA encoding 2-acyltransferase can be
CC		used to produce transgenic plants having altered lipid contents. (Updated
CC		on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct
CC		PA field.)
XX		
SQ		Sequence 374 AA;
		Query Match      75.1%; Score 1453.5; DB 2; Length 374;
		Best Local Similarity 70.9%; Pred. No. 1.5e-143;
		Matches 266; Conservative 50; Mismatches 58; Indels 1; Gaps 1;
QY	1	MAIAAAAVVPLGLLFFASGLLVNLIOAICVVVRPVSKSLYRRINRVVAELLWLVL 60
		:
Db	1	MAIPLVLVLPLGLLFLLSGLIVNAIQAVLFVTIRPFKSFYRINRFLAELLWLVLV 60
		:
QY	61	IDWWAGVKVQIFTDHEITFRMLCKEHALVISNRSDIDWLGVWSAQRSGLGSLAVMK 120
		:   :
Db	61	VDDWAGVKVQLHADEETYRSMGEHALIIISNRSDIDWLIGWILAQRSGLGSLAVMK 120
		:   :
QY	121	SSKFPLVIGSNWFSEYLFLERSWAKDESTLKSGIORLSDPFPFWLALFVEGTFTQAK 180
		:
Db	121	SSKFPLVIGSNWFSAEYLFLEBSWAKDEKTLKWGLQRLKDFPRFPFWLALFVEGTFTPAK 180
		:
QY	181	LAAAEYATSTGLVPVRNVLIPTKGFVS AVSHMRSFVPAIYDVTVAI PKSSAPTMLRL 240
		:
Db	181	LAAAEYAASQGLPAPRNVLIPRTKGFVS AVSIMRDFVPAIYDTTIVIPKDSQPMTMRI 240
		:
QY	241	FKGPSVHVHVKRHLMKELPDTDEAVAQCWRDIFVAKDALLDKHMAEGTFSDOELQDTG 300
		:
Db	241	LKGQSVIHVMKRHAMSEMPKSDVDVSKWCDFVAKDALDKHLATGTF-DEEIRPIG 299
		:
QY	301	RPIKSLLVVISACLWVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQE 360
		:
Db	300	RPVKSLLVTLFWSCLLLFGAIEFFKWTQLLSTWRGVAFSTAAGMALVTGMVHFIMFSQAE 359
		:
QY	361	RSNPAKIVPAKSKNK 375
		:
Db	360	RSSSARAARNRVKKE 374
		:
RESULT 9		
AAU00667		
ID	AAU00667	standard; protein; 374 AA.
XX		

AC	AU00667;
XX	
DT	07-SEP-2001 (first entry)
XX	
DE	Maize lysophosphatidic acid acyltransferase (LPAAT).
XX	
KW	Lysophosphatidic acid acyltransferase epsilon; LPAAT-epsilon; LPA; PA;
KW	lysophosphatidic acid; phosphatidic acid; acylation; cellular activation;
KW	phospholipid signalling; mitogenesis; inflammation; autoimmune disease;
KW	oncology; cancer; obesity; gene therapy; maize.
XX	
OS	Zea sp.
XX	
PN	WO200134782-A1.
XX	
PD	17-MAY-2001.
XX	
PF	02-NOV-2000; 2000WO-US030193.
XX	
PR	09-NOV-1999; 99US-00436919.
XX	
PA	(CELL-) CELL THERAPEUTICS INC.
XX	
PI	Leung DW;
DR	
XX	WPI; 2001-335920/35.
XX	
PT	Novel isolated human isoform of lysophosphatidic acid acyltransferase-
PT	epsilon useful for diagnostic, therapeutic and screening purposes.
XX	
PS	Example 1; Fig 2; 48pp; English.
XX	
CC	The sequence represents a maize lysophosphatidic acid acyltransferase
CC	(LPAAT) isoform, LPAAT-delta, similar to a human LPAAT isoform, LPAAT-
CC	epsilon. LPAAT catalyses the acylation of lysophosphatidic acid (LPA) to
CC	phosphatidic acid (PA). LPA and PA have been identified as phospholipid
CC	signalling molecules that affect a wide range of biological responses. PA
CC	is involved in cellular activation and mitogenesis. Compounds that block
CC	PA generation and hence diminish lipid biosynthesis and the signal
CC	involved in cell activation are of therapeutic interest in the areas of
CC	inflammation and oncology (e.g. autoimmune diseases and cancer) as well
CC	as obesity treatment. LPAAT-epsilon and its corresponding DNA can be used
CC	in screening assays to detect agents that stimulate or inhibit the
CC	activity of LPAAT and, therefore, PA. The DNA is useful in tests to
CC	detect the presence or expression of LPAAT-epsilon in relation to certain
CC	diseases and conditions, and in disease prevention and treatment. The
CC	sequences of the invention are also useful for diagnosis of diseases and
CC	conditions in which the expression of LPAAT enzyme is abnormal
XX	
SQ	Sequence 374 AA;
	Query Match 75.0%; Score 1450.5; DB 4; Length 374;
	Best Local Similarity 70.7%; Pred. No. 3.1e-143;
	Matches 265; Conservative 51; Mismatches 58; Indels 1; Gaps 1;
QY	1 MAIAAAAVVPLGLLFFASGLLVNLIQAICVVVVRPVSKSLYRRINRVVAELLWLVL 60
DB	:    :    :    :    :    :    :    :    :    :    :
DB	1 MAIPLVLVPLGLLFLISGLIVNAIQAVLFVTIRPEKSFYRRINRFLAELLWLQLVV 60
QY	61 IDWAGVKVQIFTDHETFRMLGKEHALVISNHRSDIDMLVGWVSQAQRSGCLGSTLAMVK 120
DB	:    :    :    :    :    :    :    :    :    :    :    :
DB	61 VDWAGVKVQLHADEETYRSMGKEHALIISNHRSDIDMLIGWILAQRSGCLGSTLAMVK 120
QY	121 SSKFLPVGSMWFSEYLFLERSWAKDESTLKSGIQRLSDFELFWALFVEGTRFTQAK 180
DB	:    :    :    :    :    :    :    :    :    :    :
DB	121 SSKFLPVGSMWFAEYLFLEERSWAKDEKTLKWGLQRLKDFPRFFWALFVEGTRFTPAK 180
QY	181 LLAAQEYATSTGLPVPRNVILPRTKGFSVASHMRSFVPAYDYTVTAIPKSSPAPTMLRL 240
DB	:    :    :    :    :    :    :    :    :    :    :
DB	181 LLAAQEYAASQGLPAPRNVLIPRTKGFSVSAVIMRDFVPAYDYTTVIIVPKDSPQPTMLRI 240
QY	241 FKQPSPVHVHIKRHLMKELPDTDEAVAQCWRDIFVAKDALLDKHMAGEFTSQDELQDTG 300
	:    :    :    :    :    :    :    :    :    :    :

Db 241 LKGQSVIHVRMKRHSMPKSDVSKWCKDIFVAKDALLDKHLATGTF-DEEIRPIG 299

QY 301 RPIKSLVVISWACLWVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQE 360

Db 300 RPKVSLVTLFWSCLLLFGAIEFFKWTQLLSTWRGVAFSAFGLAVVTALMQILIQFSQE 359

QY 361 RSNPAKIVPAKSKNK 375

Db 360 RSSSARAARNRVKKE 374

RESULT 10

ID AAE15288 standard; protein; 374 AA.

XX AAE15288;

AC AAE15288;

XX 07-MAR-2002 (first entry)

DE Maize LPAAT protein.

XX Lysophosphatidic acid acyltransferase; LPAAT protein; trauma;

KW 1-acyl sn-glycerol-3-phosphate acyltransferase; reoxygenation injury;

KW cellular pathway regulation; trilineage haematopoiesis; inflammation;

KW cytoinductive therapy; adult respiratory distress syndrome; hypoxia;

KW sepsis; maize.

XX Zea mays.

XX US6300487-B1.

PN 09-OCT-2001.

PD 18-DEC-1998; 98US-00215252.

PF 19-MAR-1996; 96US-00618651.

XX (CELL-) CELL THERAPEUTICS INC.

XX Leung DW, Adourel D, Hollenback D;

PI WPI; 2002-033181/04.

DR New nucleic acid encoding human lysophosphatidic acid acyltransferase, useful for identifying specific inhibitors, e.g. for inhibiting inflammation.

XX Disclosure; Fig 2; 69pp; English.

PS The present invention relates to polypeptides with lysophosphatidic acid acyltransferase (LPAAT) activity and polynucleotides encoding such polypeptides. LPAAT also referred as 1-acyl sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51), catalyses the acylation of lysophosphatidic acid (LPA) to phosphatidic acid (PA). Polypeptides of the invention are used for identifying specific modulators, potentially useful for regulating cellular pathways, e.g. to augment trilineage haematopoiesis after cytoinductive therapy or to inhibit inflammation after hypoxia and reoxygenation injury (e.g. sepsis, trauma and adult respiratory distress syndrome). The present sequence is maize LPAAT protein

XX Sequence 374 AA;

SQ Query Match 75.0%; Score 1450.5; DB 5; Length 374;

Best Local Similarity 70.7%; Pred. No. 3.1e-143;

Matches 265; Conservative 51; Mismatches 58; Indels 1; Gaps 1;

QY 1 MAIAAAAVVPLGLLPFASGLLVNLIQAIQYVVRPVSKSLYRINRVVAELWLELVWL 60

Db 1 MAIPLVLVLPGLLFLLSGLLVNAIQAVLFVIRPFSKSFYRINRFLAELLWLQLVWV 60

QY 61 IDWAGVKVQIFTHETFRMLGKHEHALVISNHRSDIDWLGVWSAQRSGCLGSLTAVMKK 120

Db 61 VDWAGVKVQLHDADETYRSMGKEHALIISNHRSDIDWLIGWILAQSGCLGSLTAVMKK 120

QY 121 SSKFLPVIGWSMWFSEYLFLEERSWAKDESTLKGIOQLSDFFPLPFWLALFVEGTRFTQAK 180

Db 121 SSKFLPVIGWSMWFSEYLFLEERSWAKDESTLKGIOQLSDFFPLPFWLALFVEGTRFTQAK 180

QY 181 LLAQAEYATSTGLPVRNVLIPTKGFVSASVSHMRSFVPAIYDVTVAPKSSPAPTMRL 240

Db 181 LLAQAEYASQGLPAPRVNLIPTKGFVSASVIMRDFVPAIYDTTIVPKDSPQPTMLRI 240

QY 241 PKGQSVVHVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTG 300

Db 241 LKGQSVIHVRMKRHSMPKSDVSKWCKDIFVAKDALLDKHLATGTF-DEEIRPIG 299

QY 301 RPIKSLVVISWACLWVAGSVKFLQWSSLLSSWKGVAFSAFGLAVVTALMQILIQFSQE 360

Db 300 RPKVSLVTLFWSCLLLFGAIEFFKWTQLLSTWRGVAFSAFGLAVVTALMQILIQFSQE 359

QY 361 RSNPAKIVPAKSKNK 375

Db 360 RSSSARAARNRVKKE 374

RESULT 11

ID AAB08477 standard; protein; 374 AA.

XX AAB08477;

AC AAB08477;

XX 20-DEC-2000 (first entry)

DE Amino acid sequence of a lysophosphatidic acid acetyltransferase.

XX Lysophosphatidic acid acetyltransferase; LPAAT; transgenic plant;

KW triacylglycerol; oil content.

XX Oryza sativa.

XX WO200049156-A2.

XX 24-AUG-2000.

XX 22-FEB-2000; 2000WO-US004526.

XX 22-FEB-1999; 99US-0121119P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

PI Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ, Ripp KG;

XX WPI; 2000-558300/51.

DR N-PSDB; AAA64199.

XX New nucleic acid fragment encoding a lysophosphatidic acid acetyltransferase (LPAAT) isozyme, useful for creating transgenic plants which encode LPAAT at higher or lower levels than normal.

PS Claim 31; Page 97-99; 102pp; English.

XX The present sequence represents a lysophosphatidic acid acetyltransferase (LPAAT) isoenzyme. The nucleic acid may be used to create transgenic plants which encode LPAAT at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found. This would have the effect of altering the level of specific triacylglycerols in those cells, for e.g. overexpression of an LPAAT similar to the maize LPAAT will result in higher oil content in the seed, stem and leaf. LPAAT chimeric genes may be used for co-suppression of genes encoding LPAAT. The polynucleotides may also be used as probes for generically and physically mapping the genes that are a part of, and as markers for traits linked to those genes

XX Sequence 374 AA;

SQ



Query Match 74.0%; Score 1431.5; DB 3; Length 374;  
Best Local Similarity 71.9%; Pred. No. 3.1e-141;  
Matches 263; Conservative 47; Mismatches 55; Indels 1; Gaps 1;

QY 1 MAIAAAAVVPLGLLFFASGLLVNLIQAICYVVRVPSKSLYRRINRVVAELLWLELVWL 60  
DB 1 MAVPLVVLPLGLLFFASGLLVNLIQAICYVVRVPSKSLYRRINRVVAELLWLELVWL 60

QY 61 IDWWAGVKVQIPTDHETFRLMGKEHALVISNHRSDIDWLVGVWSAQRSGCLGSTLAVMKK 120  
DB 61 VDWAGVKIQIQLHADDETYKAMGNEHALVISNHRSDIDWLVGVWSAQRSGCLGSTLAVMKK 120

QY 121 SSKFLPVIKSMWFSEYLFRLERSWAKDETLKSGIQRLSDFFLPFWLALFVEGTRFTQAK 180  
DB 121 SSKFLPVIKSMWFSEYLFRLERSWAKDETLKSGIQRLSDFFLPFWLALFVEGTRFTQAK 180

QY 181 LLAQEQYATSTGLPVRNVLIPTKGFVSVMRSHRSDIDWLVGVWSAQRSGCLGSTLAVMKK 240  
DB 181 LLAQEQYAVSQGLPAPRNVLIPTKGFVSVMRSHRSDIDWLVGVWSAQRSGCLGSTLAVMKK 240

QY 241 FKQPSVVHVHIKRLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQDELQDTG 300  
DB 241 LKQSSVVHVIRKRMHSEMPKSEDDVSKWCKDIFVAKDALLDKHMAEGTFSQDELQDTG 300

QY 301 RPIKSLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMQILIQFSQSE 360  
DB 300 RPKVSLVLFWSCLLLYGAVKLFVLTQLLSTWKGVGFTGLGLAVVTAVMHVFMFSQSE 359

QY 361 RSNPAK 366  
DB 360 RSSSAK 365

RESULT 12  
AAB08479  
ID AAB08479 standard; protein; 374 AA.  
XX AAB08479;  
AC AAB08479;  
DT 20-DEC-2000 (first entry)  
DE Amino acid sequence of a lysophosphatidic acid acetyltransferase.  
KW Lysophosphatidic acid acetyltransferase; LPAAT; transgenic plant;  
KW triacylglycerol; oil content.  
XX Triticum aestivum.  
XX WO200049156-A2.  
XX 24-AUG-2000.  
XX 22-FEB-2000; 2000WO-US004526.  
XX 22-FEB-1999; 99US-0121119P.  
XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ, Ripp KG;  
XX WPI; 2000-558300/51.  
XX N-PSDB; AAA64201.

New nucleic acid fragment encoding a lysophosphatidic acid acetyltransferase (LPAAT) isozyme, useful for creating transgenic plants which encode LPAAT at higher or lower levels than normal.

PS Claim 31; Page 101-102; 102pp; English.

CC The present sequence represents a lysophosphatidic acid acetyltransferase (LPAAT) isoenzyme. The nucleic acid may be used to create transgenic plants which encode LPAAT at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found.

CC This would have the effect of altering the level of specific triacylglycerols in those cells, for e.g. overexpression of an LPAAT similar to the maize LPAAT will result in higher oil content in the seed, stem and leaf. LPAAT chimeric genes may be used for co-suppression of genes encoding LPAAT. The polynucleotides may also be used as probes for genetically and physically mapping the genes that are a part of, and as markers for traits linked to those genes

XX

SQ Sequence 374 AA;

Query Match 73.1%; Score 1414.5; DB 3; Length 374;  
Best Local Similarity 71.0%; Pred. No. 1.9e-139;  
Matches 260; Conservative 52; Mismatches 53; Indels 1; Gaps 1;

QY 1 MAIAAAAVVPLGLLFFASGLLVNLIQAICYVVRVPSKSLYRRINRVVAELLWLELVWL 60  
DB 1 MAIPLVLVPLGLLFFASGLLVNLIQAICYVVRVPSKSLYRRINRVVAELLWLELVWL 60

QY 61 IDWWAGVKVQIPTDHETFRLMGKEHALVISNHRSDIDWLVGVWSAQRSGCLGSTLAVMKK 120  
DB 61 VDWAGIKVQVIADPETWKLKMGKEHALVISNHRSDIDWLVGVWSAQRSGCLGSTLAVMKK 120

QY 121 SSKFLPVIKSMWFSEYLFRLERSWAKDETLKSGIQRLSDFFLPFWLALFVEGTRFTQAK 180  
DB 121 SSKFLPVIKSMWFSEYLFRLERSWAKDETLKSGIQRLSDFFLPFWLALFVEGTRFTQAK 180

QY 181 LLAQEQYATSTGLPVRNVLIPTKGFVSVMRSHRSDIDWLVGVWSAQRSGCLGSTLAVMKK 240  
DB 181 LLAQEQYAVSQGLTAPRNVLIPTKGFVSVMRSHRSDIDWLVGVWSAQRSGCLGSTLAVMKK 240

QY 241 FKQPSVVHVHIKRLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSQDELQDTG 300  
DB 241 LKQSSVVHVIRKRMHSEMPKSEDDVSKWCKDIFVAKDALLDKHMAEGTFSQDELQDTG 300

QY 301 RPIKSLVVISWACLVVAGSVKFLQWSSLLSSWKGVAFAFGLAVVTALMQILIQFSQSE 360  
DB 300 RPKVSLVLFWSCLLLYGAVKLFVLTQLLSTWKGVGFTGLGLAVVTAVMHVFMFSQAE 359

QY 361 RSNPAK 366  
DB 360 RSSSAK 365

RESULT 13  
AAG31583  
ID AAG31583 standard; protein; 376 AA.  
XX AAG31583;  
AC AAG31583;  
DT 17-OCT-2000 (first entry)  
XX Arabidopsis thaliana protein fragment SEQ ID NO: 37953.  
DE Arabidopsis thaliana.  
XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX Arabidopsis thaliana.  
XX EP1033405-A2.  
XX 06-SEP-2000.  
XX 25-FEB-2000; 2000EP-00301439.  
XX 25-FEB-1999; 99US-0121825P.  
XX 05-MAR-1999; 99US-0123180P.  
XX 09-MAR-1999; 99US-0123548P.  
XX 23-MAR-1999; 99US-0125788P.  
XX 25-MAR-1999; 99US-0126264P.  
XX 29-MAR-1999; 99US-0126785P.  
XX 01-APR-1999; 99US-0127462P.  
XX 06-APR-1999; 99US-0128234P.

PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 30-APR-1999; 99US-0132407P.  
PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 06-MAY-1999; 99US-0132487P.  
PR 07-MAY-1999; 99US-0132863P.  
PR 11-MAY-1999; 99US-0134256P.  
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PR 01-JUN-1999; 99US-0137222P.  
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PR 16-JUN-1999; 99US-0139453P.  
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PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
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PR 18-JUN-1999; 99US-0139461P.  
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PR 18-JUN-1999; 99US-0139463P.  
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PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
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PR 20-JUL-1999; 99US-0144352P.  
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PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
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PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
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PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
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PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.  
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PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149929P.  
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PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
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PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
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PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 26-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161922P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 66.0%; Score 1277; DB 3; Length 376;  
Best Local Similarity 62.3%; Pred. No. 5.2e-125;  
Matches 228; Conservative 62; Mismatches 76; Indels 0; Gaps 0;

QY 1 MAIAAAVVVPLGLFFASGLLVNLIQAICYVVVRPVSKSLYRRINRVVAELLWLVL 60  
Db 1 MKIPAAALVFIPVGVLFLISGLIVNIIQLVFFIIVRPFSSLYRRINKNVAELLWLQLWL 60  
QY 61 IDWAGVKVQIPTDHTFRLMGKEHALVISNHRSDIDWLGVWSAQRSGCLGSTLAVMCK 120  
Db 61 PDWACIKINLYVDAETLELIGKEHALVLSNHRSDIDWLIGWVMAQRVGCIGSSLAIMKK 120  
QY 121 SSKFLPVIIGSMWFSEYLFRLERSWAKDESTLKSGIQLSDPPLPFWLALFVEGTRFTQAK 180  
Db 121 EAKYLPVIIGSMWFSDYIFRLERSWAKDENTLKAGFKRLEDPMTFWLALFVEGTRFTQEK 180  
QY 181 LLAAQEYATSTGLPVRNVLIPRTKGFVSASVSHMRSFVPAIYDVTVAIPKSSPAPTMLRL 240  
Db 181 LEAAQEYASIRSLPSRNVLIIPRTKGFVSASVSEIRSFPAIYDCTLTVHNNQPTPTLLRM 240  
QY 241 PKQPSVVHVHVKRHLMKELPDTDEAVAQWCRDIFVAKDALLDKHMAEGTFSDQELQDTG 300  
Db 241 FSGQSEINLQWRHKMSELPESTDGIAQCQDLFITKDALEKYFTKDFVSDLEVHQIN 300  
QY 301 RPIKSLLVISWACLVAAGSVKFLQWSSLLSSWKGVAFSAGLAVVTALMQILIQFSQSE 360  
Db 301 RPIKPLIVVILWGLFLVFGGFKLQWLSIVASWKIILLFVFFLVIAITINQILIQSSSQ 360  
QY 361 RSNPAK 366  
Db 361 RSTPAK 366

RESULT 14  
AAG51311  
ID AAG51311 standard; protein; 310 AA.  
XX  
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XX  
DT 18-OCT-2000 (first entry)  
XX  
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XX  
KW protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

XX  
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XX  
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Query Match	Score 1246;	DB 3;	Length 310;
64.4%			

Query match 04.4%; score 1240; DD 3;  
Best Local Similarity 78.6%; pred. No. 7.1e-122;

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Matches 231;	Conservative	30;	Mismatches 33;
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QY	81	MGKEHALVISNHRSDIDWLGVGVSAQRSGCGLGSTLAVMKKSSKFLPVI	140
Db	1	MGKEHALVVCNHRSDIDWLGVWILAQSRGCGLSALAVMKKSSKFLPVI	60
QY	141	ERSWAKDESTLKSQIORLSDFFLPFWLALFVEGTRFTQAKLLAAQ	200
Db	61	ERNWAKDESTLKSGLQRLSDFFRPFWLALFVEGTRFTEAKLAAQ	120
QY	201	IPRTKGFVS AVSNMRSFVPAIYDVTVAIPKSSPAPTMLELFGQPS	260
Db	121	IPRTKGFVS AVSNMRSFVPAIYDMVTVTIPKTSPPPTMLELFGQPS	180
QY	261	PDTDEAVAQWCRDIFVAKDALLDKDMAEGTFSDQELQDTCRPIKSL	320
Db	181	PESDDAIAQWCRDQFVAKDALLDKHIAADTFPGQEQONICRPIKSL	240
QY	321	VKFLQWSSLLSSKGVAFSAFGLAVVTALMOTLIQFSQSRSNPAKIV	374
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RESULT 15

AAG13220

AAG13220  
 ID AAG13220 standard; protein; 310 AA.

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Query Match 64.1%; Score 1240; DB 3; Length 310;  
Best Local Similarity 78.2%; Pred. No. 3e-121;  
Matches 230; Conservative 30; Mismatches 34; Indels 0; Gaps 0;

QY 81 MGKEHALVISNHRSDIDLVGVNSAORSGLSTLAVMKSSKFLPVIGSMWFSEYLF 140  
Db 1 MGKEHALVVCNHRSDIDLVGVNLAQRSGLSALAVMKSSKFLPVIGSMWFSEYLF 60

QY 141 ERSWAKDESTLKSGLQSLDFPLPEWLALFVEGTRFTQAKLAAQYATSTGLPVPRNVL 200  
Db 61 ERNWKDESTLKSGLQSLDFPLPEWLALFVEGTRFTQAKLAAQYASSELPIPRNVL 120

QY 201 IPRTKGFVSVMRSFVPAIYDVTVAIPKSPAPTMRLFRKQPSVVHVHIKRLMKEL 260  
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QY 261 PDTDEAVACWCRDIFVAKDALLDKHNAEGTFSQDELQDTGRPIKSLLVVISWACLVVAGS 320  
Db 181 PESDDATAQWCRDQFVAKDALLDKHIAADTFPGQEQNIGRPIKSLAVLVLSWACVLTIGA 240

QY 321 VKFLQWSSLLSSWKGVAFSAFGLAVVTALMQIILIQFSQSERSNPAKIVPAKSKN 374  
Db 241 IKFLHWAQLFSSWKGITISALGLGIITLCMQIILIRSSQSERSTPAKVVPAPKPD 294

Search completed: July 7, 2004, 13:39:50  
Job time : 62 secs